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SEQUENCE LISTING

(i) APPLICANT:

(A) NAME: ZENECA LIMITED

(B) STREET: 15 STANHOPE GATE (C) CITY: LONDON

(D) STATE: LONDON

(E) COUNTRY: UNITED KINGDOM

(F) POSTAL CODE (ZIP): W1Y 6LN

(ii) TITLE OF INVENTION: GENETIC CONTROL OF FRUIT RIPENING

(iii) NUMBER OF SEQUENCES: 57

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(v) CURRENT APPLICATION DATA: APPLICATION NUMBER: GB PPD

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 785 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:

(B) CLONE: U-U9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

45	CGGCACGAGG	AAAAACTANG	TGAGAANGAG	ATAATCGTTG	ACCGAGGNAG	AGAATGGCGA	60
-3	GCGAGAAGAG	CAAAATCCTG	ATCATCGGGG	GCACCGGGTA	CATCGGCAAG	TTCATCGTGT	120
50	TTGCGAGCGC	CAGGTTAGGT	AACCCTACCT	TCGCTCTCGT	CCGGAGCACC	ACCGCCCCCG	180
30	CCGGCCAACC	CGAGAAGGCC	AAGCTCCTGA	GCGACTTCCA	GGCCGCCGGC	GTCACCCTCG	240
	TCCAGGGGGA	TATNTATAAC	CACGAGAGTC	TGGTTAAGGC	GATCAAGCTG	GTGGATGTGG	300
55	TCATCTCCCC	CGTCGGCTTC	GGGCANCTGA	NTGATCAGAC	CAAGATCATC	GACGCCATCN	360
	AANAAGCCGG	AGGACACATC	AAGAGGTACC	TTCCATCGGA	GTTTGGCAAC	GACGTANACC	420
60	GAAGCCATGC	TGTGGAGCCA	GCAAAGTCTA	CCTTTGTCGT	CAAGCAACAA	ATCANAAGGG	480
00	CTGTTGAGGC	ATCGGGTNTC	CCTTACACCT	TTGTATCTTC	CAACTTTCTT	CGGTGGGTNT	540
	TTCCTCCCGG	TATTATGACA	GGCAGGAGCC	ACTGGTCCTC	CCACGGACAA	GGTTGTCATC	600
65	TTAGGTNACG	GGAACNCAAA	ACGATCTTCT	CNATGAANAC	GACTTCCGGA	CATCCCATTT	660
	ANTCTTGGAT	GATCCATAAC	CTGAACCAGG	TTCTATTTCT	TAAAACTTCC	NCCACTTCTT	720
70	NTCTCTTANC	ANCTCNTTTC	CCTCTTGGGA	AAAAAATGTC	NNCTANACTT	CNAAAAGGGT	780
, 0	TTANT						785

(2) INFORMATION FOR SEQ ID NO: 2:



5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 813 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
10	(ii) MOLECULE TYPE: cDNA	
15	(vii) IMMEDIATE SOURCE: (B) CLONE: U-U17	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:	
20	CGCGCACGAG GAAGAAAACT AGGTGAGAAN GAGATAATCG TTGACCGAGG NAGAGAATGG	6
[]	CGAGCGAGAA GAGCAAAATC CTGATCATCG GGGGCACCGG GTACATCGGC AAGTTCATCG	12
\[] \25	TGTTTGCGAG CGCCAGGTTA GGTAACCCTA CCTTCGCTCT CGTCCGGAGC ACCACCGCCC	18
Ci i	CCGCCGGCCA ACCCGAGAAG GCCAAGCTCC TGAGCGACTT CCAGGCCGCC GGCGTCACCC	24
Part Street	TCGTCCAGGG GGATATATAT AACCACGAGA GTCTGGTTAA GGCGATCAAG CTGGTGGATG	30
130	TGGTCATCTC CCCCGTCGGC TTCGGGCANC TGANTGATCA GACCAAGATC ATCGACGCCA	36
i i i	TCAAAGAAGC CGGAGGACAC ATCAAGAGGT ACCTTCCATC GGAGTTTGGC AACGACGTAN	42
	ACCGAAGCCA TGCTGTGGAG CCAGCAAAGT CGACCTTTGT CGTCAAGCAA CAAATCANAA	480
.35 ∏	GGGCTGTTGA GGCATCGGGT ATCCCTTACA CCTTTGTATC TTCCAACTTC TTCGGTGGGT	540
	NTTTCCTCCC GGTATTANGA CAGGCAGGAG CCACTGGTCC TCCCACGGAC AAGGTTGTCA	600
40	TCTTANGTGA CGGGAACACA AAAGCGATCT TTCTCAATGA ANACACATCC GGACNTNCAC	660
	NATTAAAGCA GTGGATGATC CGAAAACCTG AACANGTTCT ATATCTGAAA CCTTCCGCCA	720
45	CTCTTGTCTC ATNACAACTC ATTTCCCTCT GGGAAAAAAA NGTCNGCAAA ACTCCNAAAA	780
-	GGTCTACTTC CCGGAAGAAA AATCTGAANC ANA	813
	(2) INFORMATION FOR SEQ ID NO: 3:	
50	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 746 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: unknown	
<i>JJ</i>	(ii) MOLECULE TYPE: cDNA	
60	(vii) IMMEDIATE SOURCE: (B) CLONE: U-U66	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:	
65	GGCACGAGGG GAAAAGGAGA TNATCGTTGA CCGAGGAGAG AATGGCGAGC GAGAAGAGCA	60
	AGATCCTGAT CATCGGGGGC ACGGGGTACA TCGGCAAGTT CATCGTGTTT GCGAGCGCCA	120
70	GGTTAGGTAA CCCTACCTTC GCTCTCGTCC GGAGCACCAC CGCCCCCGCC GGCCAACCCG	180

	AGAGGGCAA GCTCCTGAGC GACTTCCAGG CCGCCGGCGT CACCCTGGTC CAGGGGGGATA	240
	TATATAACCA CNAGAGTCTG GTTAAGGCGA TCAAGCTGGT GGATGTGGTC ATCTCCCCCG	300
5	TCGGCTTCGG GCAGCTGAGT GATCAGACTA AGATCATCGA CGCCATCAAA GAAAGCCGGA	360
	GGACACATCA AGAGGTACCT TCCATCGGGA GTTTGGCAAC GACGTANACC GAAGCCATGC	420
10	TGTGGAAGCC ANCAAAGTCG ACCTTTGTCG TCAAGCAACA AATTANAAGG GCTGTTGAGG	480
10	CATCGGGGAT CCCTTACACC TTTGTTATCT TCCAACTTCT TCGGTGGGTA TNTCCTCCCC	540
	GTATTGGGAC AGGCANGAAC CACTGGTCCT CCCCACGGAC AAGGTTGTCN TCTTAGGTGA	600
15	ACGGGAACAC CAANGCGATC TTTCTCAATG AAAGACAACT CGGGACATNC CCNATTTAAC	660
	CANTGGATGA TCCNANAACC TGAACAAGGT CTATTTCTGA AAACTTCNCC ATCTTCTTTT	720
20	TCTCATAACG AACCCNTTTN CCTCTT	746
20	(2) INFORMATION FOR SEQ ID NO: 4:	
1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 795 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: unknown	
[(30 [[]	(ii) MOLECULE TYPE: cDNA	
135 135	(vii) IMMEDIATE SOURCE: (B) CLONE: U-U104	
ru.	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:	
(() (:4 0	GGCACGAGGA AANGAGATAA TCGTTGACCG AGGCAGAGAA TGGCGAGCGA GAAGAGCAAA	60
ļ-l-	ATCCTGATCA TCGGGGGCAC CGGGTACATC GGCAAGTTCA TCGTGTTTGC GAGCGCCAGG	120
	TTAGGTAACC CTACCTTCGC TCTCGTCCGG AGCACCACCG CCCCCGCCGG CCAACCCGAG	180
45	AAGGCCAAGC TCCTGAGCGA CTTCCAGGCC GCCGGCGTCA CCCTCGTCCA GGGGGATATA	240
	TATAACCACG AGAGTCTGGT TAAGGCGATC AAGCTGGTGG ATGTGGTCAT CTCCCCGTC	300
50	GGCTTCGGGC AGCTGAGTGA TCAGACCAAG ATCATCGACG CCATCAAAGA AGCCGGAGGA	360
30	CACATCAAGA GGTACCTTCC ATCGGGAGTT TGGCAACGAC GTTANACCGA AGCCATGCTG	420
	TGGAGCCAGC AAAGTCNACC TTTGTCGTCA AGCAACAAAT CANAAGGGCT GTTGANGCAT	480
55	CGGGTNTCCC TTACACCTTT GTATCTTCCA ACTTCTTCGG TGGGTATTTC CTCCCGGTAT	540
	TANGACAGGC AGGACCACTG GTCCTCCCCA CNGACAAGGT TGTCNTCTTA GGTGACNGGA	600
60	ACACAAAANC ATCTTTCTCN ATGAAGACAA CTCCGGACAT ACNCNATTAA AGCNGTGGAT	660
30	GATCCCAAAA CCTGAACAAG TTCCTATNTC TTGAAAACTT TCCCGCCCAA CCATCCTTTN	720
	GTTCTCCCNT TAAACCNAAC CTCCATTTTC CCCTCCTTGG GGAAAAAAAA AAGGTCCGGC	780
65	NAANAACTTC CNAAA	795

⁽²⁾ INFORMATION FOR SEQ ID NO: 5:

⁽i) SEQUENCE CHARACTERISTICS:

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_	(A) LENGTH: 797 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: unknown	
5	(ii) MOLECULE TYPE: cDNA	
10	(vii) IMMEDIATE SOURCE: (B) CLONE: U-U13	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:	
13	CGGCACGAGG NAGAACCTTT TGACAGAGTT GTTGTCATGG CAACAAAAGC TTCTCTCTC	60
	ATAAAAGGCT TTGCCTTGCT GGTTTCAGTC CTTGTAGCAG TTCCAACAAG AGTGCAATCG	120
€ 20	ATTGGTGTCT GCTACGGCAT GCTCGGCAAC AATCTTCCCC CGCCCAGCGA GGTGGTCAGT	180
74. 27. 10.14 10.11 10.14 10.11	CTCTACAAAT CCAACAACAT CGCGAGGATG AGACTCTACG ATCCAAACCA AGCCGCCCTG	240
QT ·	CAAGCCCTCA GGAACTCCAA CATCCAAGTC CTGTTGGATG TCCCCCGATC CGACGTGCAG	300
(125 (1)	TCACTGGCCT CCAATCCTTC GGCCGCCGGC GACTGGATCC GGAGGAACGT CGTCGCCTAC	360
	TGGCCCAGCG TCTCCTTTCG ATACATAGCT GTCGGAAACG AGCTGATCCC CGGATCGGAT	420
å≥k 30	CTGGCGCAGT ACATCCTCCC CGCCATGCGC AACATCTACA ATGCTTTGTC CTCGGCTGGC	480
	CTGCAAAACC AGATCAAGGT CTCGACCGCG GTCGACACGG GCGTCCTCGG CACGTCCTAC	540
	CCTCCCTCCG CCGGCGCCTT CTCCTCCGCC GCCCAGGCGT TACCTGANCC CCATCGTGCA	600
1135	GTTCTTGGCG ANTAACGGAA CGCCGCTCCT GGTCAATGTG TACCTTATTT TAACTACACC	660
### ###	GGCAACCCGG GANAGATCTC GCTGCCTACN CCCTGTTCAC GGCCNCGGGG TCTCNTGCAG	720
40	GATGGGCGAA TTCCNCTATC ANAANCTGTT CANTCCATCT TCNAAACCGG TCTTCCCGGG	780
	CTGGAAAAA TTGGAAG	797
	(2) INFORMATION FOR SEQ ID NO: 6:	
45	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 792 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	
50	(D) TOPOLOGY: unknown	
	(ii) MOLECULE TYPE: cDNA	
55	(vii) IMMEDIATE SOURCE: (B) CLONE: U-U136	
60	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:	
	GGCACGAGGA GAACCCTTTT GACAGAGTTG TTGTCATGGC AACAAAAGCT TCTCTCTCA	60
65	TAAAAGGCTT TGCCTTGCTG GTTTCAGTCC TTGTAGCAGT TCCAACAAGA GTGCAATCGA	120

TTGGTGTCTG CTACGGAATG CTCGGCAACA ATCTTCCCCC GCCCAGCGAG GTGGTCAGTC

TCTACAAATC CAACAACATC GCGAGGATGA GACTCTACGA TCCAAACCAG GCCGCCCTGC

AAGCCCTCAG GAACTCCAAC ATCCAAGTCC TGTTGGATGT CCCCCGATCC GACGTGCAGT

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	CACTGGCCTC CAATCCTTCG GCCGCCGGCG ACTGGATCCG GAGGGAACGT CGTCGCCTAC	360
	TGGCCCAGCG TCTCCTTTCG ATACATAGCT GTCGGAAACG ANCTGATCCC CGGATCGGAT	420
5	CTGGCGCAGT ACATCCTCCC CGCCATGCGC AACATCTACA ATGCTTTGTC CTCGGCTGGC	480
	CTGCAAAACC AGATCAAGGT CTCCGACCGC GGTCGACACG GGCGTCCTCG GCACGTCCTA	540
10	CCCTCCCTCC CGCCGGNGCC TTCTCCTCCG CCGCCCAAGC GTNCTGANCC CCATCGTGCA	600
10	NTTCTTTGGC GAAATAACGG ANCGCCGCTC CCNGGTCCAT GTTTTTCCCT TATTTTAACT	660
	ACNCCGGCAA CCCNGGAAAG ATTTCGCTGC CCTTACGCCC CCTGGTTTCC NNGGGGCTTC	720
15	CCGGGCGTTT CTTCCTTTGC CAGGGANTNG GGGCGAATTC CCNNCTTTTC CANAAACCTT	780
	GTTCCAACNC CC	792
55%	(2) INFORMATION FOR SEQ ID NO: 7:	
120 11 11 125	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 855 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
	(ii) MOLECULE TYPE: cDNA	
30	(vii) IMMEDIATE SOURCE: (B) CLONE: U-U21	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:	
	CGGCACGAGT CTCTCTGT CTCTCCGTCG TCTCGTTGTC TGTTCGTTAG GGCTTGCGAT .	60
40	CGCCACCGGT CGCGAGGGTT GGAGCCATGG AATTCTTGCG GTTTGGGGCT GAGGTGGCGG	120
	CAGGAGAGA AGCCGCGACG GGGTACTGGA TGCGATGGCA GACGCTCGTC TGCGCTCTGA	180
• • =	TCGTCGTCGC CCCGGCGGTC GCCGCGGTGG TTGTCGCGGC-GCGGGCGCCG GCGCCGGCGC	240
45	GACCGCTCAG GGCCGTCGAT CTCTGGGCGC CGTGCTGGGC CGGGATGCAC CCGGCCTGGC	300
	TTCTCGCGTA CCGCGGCTTC NTGTTCTTGG CCATGGCGTG GCTACTCTTC CANATGATTC	360
50	TGTTTCGCGG ATTCTCCGCG TTCTACTTCT ATACTCAGTG GACGTTTGCC TTAGTCATTG	420
	TCTATTTTGC GATCGCAACC ATTATATCCG CCCATGGCTG CTGGCTTTAC TCAAAGAGAA	480
	GTATTATGCC AGATCAGGAG GTCAACAGAT TCCTAAATGG TGGTTTTGAG CANAATAGTC	540
55 -	CTATGACTCT ACCTTTGAGG ACCAACAAAA ATATGAATGT TATAAGATTG CAAAGCTATC	600
	NTGAACAGGA NGCTGATGAA NAAAAANCTG GATTTTGGGG TCCTGCTATG CNACTNGTCT	660
60	ATCAAAACCA TTGCANGTGC TGTAATTGTT GAAANACATT GTATTTTGGG NTCNTNCTAA	720
50	TACCATATTT GTCTTCTATA AATTTCAGGC TAAATGCTAT AATGGGCTGC ATGCATTCTC	780
	TTAATGCTGT GTTTCTTCNA ATCCAACACT TTTCTCAATA ACCTGCCATT CCCNTNTTTC	840

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(2) INFORMATION FOR SEQ ID NO: 8:

NAATGGCATT TTTGC

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 722 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

5	(11) MOLECULE TYPE: CDNA	
	(vii) IMMEDIATE SOURCE: (B) CLONE: U-U31	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:	-
15	CGGCACGAGA GAGAGAGAG GAGAGAGAGA GAGAGAGA	60
13	GAGAGAGAC CTAGACCGGC ATCNTCGTGC TTGCCGAGGG GCGGCTTATG ANTCTTGGTT	120
	GTGCCACTGG GCATCCCAGC TTCGTCNTGT CCTGCTCCTT CACCANCCAN GTGATNGCAC	180
20	NACTGGANTT ATGGANGGAA ANGGCGACCG GCNNGTACGA NAAGAANGTC TATGTGCTGC	240
# F E	CCANGENTET GGATGAGAGG GTGGENGEGE TECNEETEGG CAAGETGGGT GEENEGETEA	-300
	CCNAGCTTAC NCCNTCGCGG GCTGATTACA TTAGCGTCCC GATCGAGGGA CCCTACANGC	. 360
125 111	CTGCTCACTA CNGGTATTNG GGTTGCTTNT GCNAGAGACG ATGATNATAN NTCGGAGCAC	420
444 444 444 444	TGGCNTTTTC GACTANNAGT TTGACCGATG GCTATGTTCG TTTTGCTTTT CACCTTTTGT	480
30	CTTCCCATCT TTGCTGGTTC ACCTATGGAC GTTTGTTCCA TTTGGATGTN NTGAGAAATG	540
3 3	CTGATGGCAT TTTCGGAAAN AAAAANATNT AAAATCNCGA GAGTTCTTCT ANAGCGGCCG	600
11	CGGGCCCNTC NNTTTTCCCC CGGGTGGGGT ACCANGTTTG TTGTNCCCNT TCCCCCTNTT	660
3 5	TGAGTCCTTT TACTNCCCCT GGCCGTCGTT TTATACNTCG TTGACTGGGA ANACCCTGCC	720
EL)	NT	722
<u>40</u>	(2) INFORMATION FOR SEQ ID NO: 9:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 793 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D)- TOPOLOGY:-unknown	
	(ii) MOLECULE TYPE: cDNA	
50	(vii) IMMEDIATE SOURCE: (B) CLONE: U-U131	
·55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:	
	GGCACGAGCC TTGCCCAACT CCTTCGATTC GTTCCAACGA TCGGAGAATG GCGCTGCTGG	60
60	TGGAGAANAC GTCGACGGGA CGCGAGTACA AGGTGAAGGA CCTTTCTCAG GCTGACTTCG	120
	GCCGCCTCGA GATCGAGCTG GCGGAGGTGG AGATGCCGGG CCTCATGGCG TGCCGCGCCG	180
65	AGTTCGGGCC CGCCAAACCT TTCGCCGGCG CCCGCATCTC CGGCTCCCTC CACATGACCA	240
	TCCAGACCGC CGTCCTCATC GAGACCCTCA CCGCCCTCGG TGCTGAAGTC CGGTGGTGCT	300
	CCTGCAACAT CTTCTCCACC CAGGACCACG CCGCTGCCGC CATTGCCCGC GACTCCGCCG	360
70	COSTITUCE CTOCARCES GAGACCETCS COGAGTACTS STEETCACE GAGCGATGCC	420

TCGACTGGGG CCCCAACGGT GGCCCCGACC TCATCGTCGA CAAAGGGGGT GACGCCACTC

	TCCTCATCCA CGAAGGCGTC AAGGCTGANG AAGANTACGA AAAAGACCGG CAAGCTGCCC	540
5	GATCCGGCCT CCACGGAAAA CGCCGAATTC CAAATCGTGC TGGGGATTAT CCGCNANCGG	600
	CTCCAGGTCN AACCCCNAAA ATTACCGCCC AGATNAAAGA ACCCTCCTCC GCTTTTTGAA	660
10	GAAAACANCN CTGGCGTTCA NCGAATCTAC CANATGCCAG GGCCANCNGG GGCCCCTTGC	720
.10	TTCTTTCCCC CCNCCCANTC NAACNTTCCN ACGAATTCCC GTTTTACCCN AAAAACCAAN	780
	TTTTGAACAA CCT	793
15	(2) INFORMATION FOR SEQ ID NO: 10:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 847 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
10 10	(ii) MOLECULE TYPE: cDNA	
25 L	(vii) IMMEDIATE SOURCE: (B) CLONE: U-U32	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:	
L[]	CGGCACGAGG CGACGCCGGC CTTCGCCTCC GCGTCTCCCT CCACCTCCAC TGCCACCGCC	60
[U35 [U	GCCCTCGCCT CCCCCTCCCC AAATCGGTCG ACTCCGCCGC CGCTACAGAC CCCGACATCC	120
	TATTCACTGA CCGCCGCCGGC CGCCGCCGTG CCGACTGCCT CTCCTTCGCT GTCGACGACC	180
40	TCCCTGTCCT CGACGGCAGG ACCCCGATGG AAGCCTACGA GGAGTTCTTC CGGAGCTTCC	240
	GCCTCGCCTT CGCTGACTTC TTTGGTTCCG TCATTACGGA TATCACGATC GGTCTCGGGC	300
-0	CAAATGCCGA GCTCCGTTAC CCTTCGTTTC CTCCCACTGG AAGCAATCGT TTCACCGGTG	360
45	TAGGAGAATT CCAGTGTTAT GACAAATACA TGCTTGCCGA TCTCAAACGA CACGCGGAGG	420
	AAACCGGCAG CCCATTATGG GGCCTCTCTG GTCCTCACGA TGCCCCTGGG TACAACCAGT	480
50	CTCCGGACTT CGGCAACTTT TTCAAGGACC ATGGCGGCTC CTGGGANACA CCCTACGGGC	540
	AATTCTTCCT CTCCTGGTAC ACCGGCAAGC TCCTGTCTCA CGGTGACGGC CTGCTCTCGG	600
	TCGCGTCAGA AGTATTGGTG ATTTGCCTGT CGCGCTCTCG GGCAAGGTTC CACTTTCTGC	660
55	ATTTGTTGGC AACGAAACTC GGTCGCGCCC GTCTTANCTT GAAGGCCGGG TTCTNTNACA	720
	CTTGACGGNA NAANAACNGG TTTCAAGGAT GTTGGCTAAN ATCTCCCGAA ANCNTCCTGC	780
60	ANCATGATTC ATCCCGGGCN TGGACTTCTC NGAAGGGGAA CANTCCTCAG GGTGTTCCGG	840
	TCTGCCC	847
	(2) INFORMATION FOR SEQ ID NO: 11:	
70	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 822 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown	

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE: (B) CLONE: U-U55

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:	
10	GGCACGAGGC ATGGAGAACC CTGTTGCGAT GGGCATCATG GAGGAGCTTG AGGCCCAGAG	60
	CGAGGTGTGG AACCACATTT TTAGATTCAT CACCTCCATG TCCGTCAAGT GCGCGGTGGA	120
15	GCTCAGGGTC CCCGACGCCA TCCACGCCCA CGGCGGCAAC GCAACTCTCC CTCAGCTGGC	180
13	CGCCGCCCTC AGCCTCCCTC CCGCCAAGCT CGCCGACCTC CGACGCCTCA TGCGCATGCT	240
	GGTCCACGCC GGCTGCTTCG CCAAGCAGGA AGACNACGTG TACGCCCTCA CGCCATGGTC	300
20 []	GAGGCTCCTG NTGAGCTCCG AGCACACCGC GGTAGCCCCG TTCGTGGTGT GGATGCTCCA	360
ŧij.	CCCGCTCATG GTGCAGTCGT GGCACTCGCT GGGGGCGTGG TTCCACGGGA GGGCGCCCAC	420
11 1125	CCCCTTCGCC GCAACCCACG GGAAAGGGGA TCTTCGAGAC NACACNCNAA CAGCCGGGGT	480
	TCGCGGCCGT TCTTCANCNA NGCNATGGCG AACGACTGTC GGCTGGTGGG AAAGGTGTTG	540
Harry Control	GTAAANAACA TNCGGATGTG TTGGANGGAN CNCNGGTCCA TNGTGGAAGT TGGTGGCGCA	600
<u>}</u> 30	CCGGCACCCT TTTNGGCCAT TGTTGGCCGA AGGCTTTCCC GCCAACATNA AATNGCACCG	660
	TTCTCCNANT TTGCCCCACT TTTCTGGCCN CNGCCGCCGG GGCCCCCNCN NACCNAAACA	720
113	ACTTGGATGT TTTTNGGGGG AANACATNTT CCAACATTTT ACANCCGCNC GACNTTTTTT	780
1135 111	ACNCAATTGG TTCCNGGCNC NAATGGAAAT ANTNCTGNAT TT	822
	(2) INFORMATION FOR SEQ ID NO: 12:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 743 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	

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(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE: (B) CLONE: U-U72

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12: 55 GGCACGAAGA GCCCTGTACC GGANAGCATG GAGAACCCTG TTGCGGTGGG CATCATGGAG 60 GAGCTTGAGG CCCAGAGCGA GGTGTGGAAC CACATTTTTA GATTCATCAC CTCCATGTCC 120 60 GTCAAGTGCG CGGTGGAGCT CAGGGTCCCC GACGCCATCC ACGCCCACGG CGGCAACGCA 180 ACTCTCCCTC AGCTGGCCGC CGCCGTCAGC CTCCCTCCCG CCAAGCTCGC CGACCTCCGA 240 CGCCTCATGC GCATGCTGGT CCACGCCGGC TGCTTCACCA AGCAGGAANA CNACGTGTNC 300 65 GCCCTCACGC CATGGTCGAN GCTCCTGGTG AGCTCCGANC ACACCTCGGT GGCCCCGTTC 360 GTGGTGTGGA TGCTCCACCC GCTCATGGTC CAGTCGTGGC ACTCNCTGGG GGCGTGGTTC 420 70 CACGGGAAGG GCGCCCACNC CCTTCNCCNC NACCCNCGGG AAGGGGATCT TCCANACGAC 480

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	ACNCGAACAT CCGGGGTTCG CGGGCGTCTT CAACTANGCG ATGGCGAACG ACTGTCNGCT	540
	GGTGGGAAAN GTNTTGGTAA AAAAACCTTC CGGAAGTGTT NGANGGAACC CCGTCCAATN	600
5	GTGGAANTTG GTGGCNGCCG GCACCCTTNC GGGCNATCGT TGTCGAAGNC CTTCCCNCAC	660
	NTTANATTNC ACCGTCCTCC AATTNTCCCC ANTTTCTTTN GCCGCNGGNN NCGGGCCCCN	720
10	GGTNANCCNA AANCNTTTNT TTT	743
10	(2) INFORMATION FOR SEQ ID NO: 13:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 806 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
20	(ii) MOLECULE TYPE: cDNA	
1 1 1 25	(vii) IMMEDIATE SOURCE: (B) CLONE: U-U68	
general genera	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:	
() () 30	TGTTCTCCC TTCGATCACA TCTTTTTGCT CTGGGAAACG TGAGAGGTGA GACGAGGGCG	60
ala a	GCAATGACGG CGGGTTTAAG ATGGATTCCT CCTCTGCTTC TTCTTCTTCT GGGCTTCCTG	120
=1	CTGGTTTTGA ACGGAGGTCG GGGGTGGATT GGAAGCGAGA GGTCCTCTGG CTCGAGGAAT	180
35	GGCGGAGCAT CGCGGAGGAG CTTGAGAGAG GCCTCCGCGA ACGCGACCAG CGCCGATGCT	240
	TCCTTGGAAG AGAGGGCTGT AACCCGGGCA GCAGAAGCCG CAGTCGACGA CCCCGAGGAG	300
40	GTTGCTTCGA CGGTCCTGAT GACCATAATC AACAGCACGG CTCGCAGATC TCTTGGTTAT	360
en .	CTGTCGTGCG GTTCAGGCAA CCCGATCGAC GACTGCTGGC GGTGCGACCC TGATTGGCAT	420
	GTCAACAGAA AAAAGCTCGC TGACTGCGGC ATTGGCTTTG GACGCAACGC NATANGTGGC	480
_45 _	CGCGACGGGG AATTTGTTCG TTGTGACAGA CTCCGGGGAC NATGATCCCC GTGAATCCTC	540
	GCCCGGGAAC ACTTANATAC CCCGTCNTCC AANGAAGTTG CCCCCTCTGG GATCCCCTTT	600
50	AAACNCNAAN TGGAAATCTC NCTCNANGGA AGAACTCNTT ATGAACAGCT TTAANACNAT	660
	CGATGGACNC NGTGTCCTCG TCCACATTGC CAATGGCGCC TGCNTCACCA NCCAATTTCN	720
	TCCCCAACNT CTTCTTCCNT NGCCTCCNCT CCCCAATGCA ACCCNCCGGG AATTCCTNGT	780
55	CCCCNCTCCC CTTCTCCTAT GGATNG	806
	(2) INFORMATION FOR SEQ ID NO: 14:	•
60	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 687 base pairs	

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

65 (ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE: (B) CLONE: U-U69

741

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:	
5	GGCACGAGGG AGAACAAAAA TGGCAGCATT CTTGTTCTTC CTCACCATCG CAGCCTTCAC	60
,	TGCCCCCATC TACTCTTCTC GTGCACCCTT AACGTCGGCA GCTGTCCGCG ACCCTGAATT	120 ·
	AGTAGTACAG GAAGTACAAA GAAGCTTGAA CGTGTCGCGG CGGCGACTGG GCTACTTGTC	180
10	ATGCGGCACC GGCAATCCGA TCGACGACTG CTGGCGGTGC GACCCTGACT GGGCTGACAA	240
	CCGGCAGCGG CTCGCGGACT GCGCCATCGG GTTCGGGAAG AACGCGATTG GGGGCAGGGA	300
15	CGGCGAGATA TACGTGGTGA CCGACAGTGG CGACNACNAC CCCGTCAATC CGAAGCCGGG	360
15	CACGCTCCGG TACGCCGTCA TCCANGAGGG AGCCGCTGTG GATCATCTTC AAGCGCGACA	420
	TGGTCATCCA GCTGAAGGAA GGAGCTCATC ATGAAACTCC CACANAGACC ATCGACGGCC	480
20	GGGGCGCCAG CGTCCACATC TCCGGGGGGC CGTGCATCAC CACCAGTNCG TCNCCAACAT	540
	CATCATCCAC GGGCGTCCAC TTCCACNAAT GCAANCAGGG CGGGGAACGC CTTACGTTCG	600
2 5	CGACTCCCCC AGGGCACTAC GGGTGGCGCA CCGGTGTCCG AACGGCNANG GGGTTTTCAT	660
71	CTTCCGCGGG AACCACTTCT GGGGTCA	687
	(2) INFORMATION FOR SEQ ID NO: 15:	
30 35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 741 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
	(ii) MOLECULE TYPE: cDNA	
4 0	(vii) IMMEDIATE SOURCE: (B) CLONE: U-U84	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15: TCCACATTGC CAATGGCGCC TGCATCACCA-TNCAGTACAT-CACCAACGTC ATCATCCATG	
	GCCTCCACAT CCACGACTGC AAGCCCACCG GGAATGCCAT GGTCCGCAGC TCTCCTTCTC	60
50	ACTATGGATG GAGAACCATG GCTGATGGGG ATGCCGTTTC CATTTTCGGC TCCAGCCACA	120
	TTTGGGTGGA CCACTGCTCT CTGTCCAACT GCGCCGATGG ACTTGTCGAT GCCGTCATGG	180
	GCTCCACTGC CATTACGGTC TCCAACAATT ACTTCACCCA CCACAATGAG GTCATGCTTT	240
55 .	TGGGACACAC TGATTCTTAT GCAAGGGACA GCATCATGCA AGTAACGATC GCATTTAACC	300
		360
60	ATTTTGGTGA AGGTCTGATT CAGAGAATGC CCAGGTGCAG GCATGGCTAC TTCCACGTGG	420
-0	TAAACAATGA CTACACGCAC TGGGAGATGT ACGCCATTGG CGGTAGCGCG AATCCAACGA	480
	TCAACAGTCA AGGCAACCGA TACCTTGCGC CGACCAATCC ATTTGCAAAG GAAGTAACAA	540
65	AAAGGGTGGA CACAGATCAA AGCACGTGGA AAAACTGGAA TTGGANGTCN GAAGGTGACC	600
	TGCTTCTGAA TGGTGCTTTT TTCACCCTTC CGGTGCANGG GCTTTCACCC ANCTACGCAC	660

GGGCCTCCAC TTTGGGGGCA ACCCTCTTCC TTNGTTGANA CACTGACTCT GATGCTGGGG

70 TCCTGTTTTG CCAATTCGGN C

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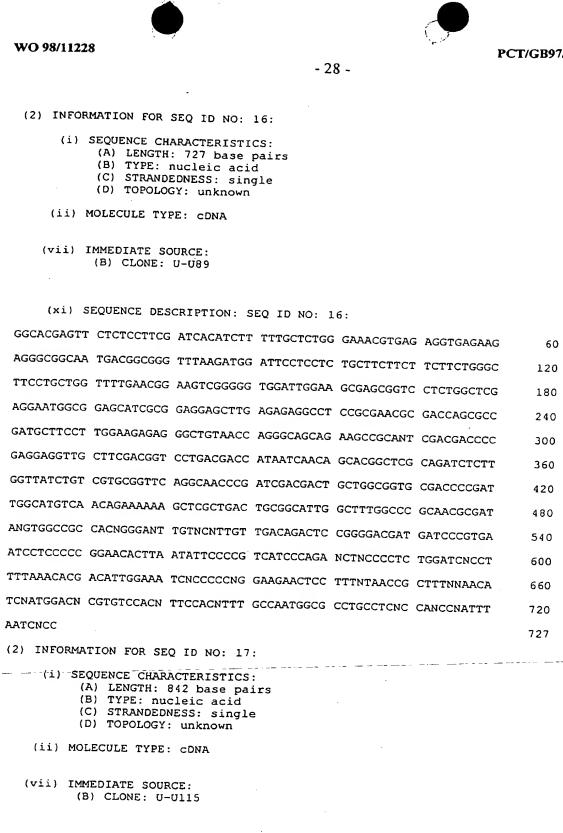
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AATCNCC



(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GGCACGAGGG AGAACAAAAA TGGCAGCATT CATGTTCTTC CTCACCATCG CAGCCTTCAC 60 65 TGCCCCCGTC TACTCTTCTC GTGCACCCTT AACGTCAGCA GCTGTCCGCG ACCCTGAATT 120 AGTAGTACAG GAAGTACAAA GAAGCTTGAA CGTGTCGCGG CGGCGACTGG GCTACTTGTC 180 ATGCGGCACC GGCAATCCGA TCGACGACTG CTGGCGGTGC GACCCTGACT GGGCTGACAA 240 70 CCGGCAGCGG CTCGCTGACT GCGCCATCGG GTTCGGGAAG AACGCGATTT GGGGCAGGGA 300

	CGGCGAGATA TACGTGGTGA CCGACAGTGG CGACNACGAC CCCGTCAATC CGAAAACGGG	360
5	CACGCTCCGG TACGCCGTCA TCCAGGAGGA GCCGCTGTGG ATCATCTTCA AGCGCGACAT	420
,	GGTCATCCAG CTGAAGGAGG AGCTCATCAT GAACTCCCAC AAGACCATCG ACGGCCGGGG	480
	CGCCAGCGTC CACATCTCCG GCGGGCCGTG CATCACCACC AGTACGTCAC CAACATCATC	540
10	ATCCACGGCG TCCACATCCA CGAATGCAAG CAGGGCGGGA ACGCGTNCGT TCGCNACTCC	600
	CCAAGGCAC TACGGGTTGG CGCACNGTGT TCNGACGGCG ACGGGTGTCC ATCTTCCGCG	660
15	GGAACCACTC TGGGTCCAAC CACTGCANCG CTTGTTCCAA CTTGGCCCAC CNAANTGGGC	720
15	CTTCCNTCCC AACCCCCATT TCCTTGGGAT TNCCCCCCGC CAATTCCCCC ATTTTCCAAC	780
	NAACTINCTI TGAACCCNCC CNTGAANAAG GTCCTTGCTG CTGGGTCCCA CCAACAATTT	840
20	NA	842
:.) ::)	(2) INFORMATION FOR SEQ ID NO: 18:	
25 11 11 13 13	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 724 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA	
35	<pre>(vii) IMMEDIATE SOURCE: (B) CLONE: U-U117 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:</pre>	
40		
	GGCACGAGTC TCCTTCGATC ACATCTTTTT GCTCTGGGAA ACGTGAGAGG TGAGACGAGG GCGGCAATGA CGGCGGGTTT AAGATGGATT CCTCCTCTGC TTCTTCTT TATGGGCTTC	60
	CTGCTGGTTT TGAACGGAGG TCGGGGGTGG ATTGGAAGCG AGAGGTCCTC TGGCTCGAGG	120
45		180
	AATGGCGGAG CATCGCGGAG GAGCTTGAGA NAGGCCTCCG CGAACGCGAC CAGCGCCGAT	240
50	GCTTCCTTGG AAGACAGGGC TGTAACCAGG GCAGCAGAAG CCGCAGTCGA TGACCCCGAG GAGGTTGCTT CGACGGTCCT GACGACCATA ATCAACAGCA CGGCTCGAAN ATCTCTTGGT	300
30	TATCTGTCGT GCGGTTCAGG CAACCCGATC GACNACTGCT GGCGGTGCGA CCCCGATTGG	360
	CATNICAACA GAAAAAAGCI CGCIGACIGI GGCATIGGCI TIGGCCGCAA CCCGATANGI	420
55	GGCCGCGACG GGGANTTGTN CGTTGTGACA GACTCCGGGG ACGATGATCC CCNTGAATCC	480 540
	TCCCCGGGA ACACTTANAT NCCCGTCNTC CNNGAANTTT CCCCTCTGGA TCNCCTTTAA	600
60	ACCCACNTGG ANATCCCCCN CNAGGAAGAA CTCCTTATGA ACNGCTTTTT AAAACATCGA	660
	TNGGACCONG TTTCCACTTC CNCATTNGCC NAATTGGGCG CCCTGGCCNT CCNCCCNTCC	720
	CCAA	724
65	(2) INFORMATION FOR SEQ ID NO: 19:	
70	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 797 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	

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420

(D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA 5 (vii) IMMEDIATE SOURCE: (B) CLONE: U-U80 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19: GGCACGAGGG ACAAGCGATG GCAGCAGAAT TGTCTCCCAC GCTGAGCAAG AGCATCTTTG 60 15 AAGGAGCCGG TGGATCTTAC TCTACTTGGT CAGGTGCCGA TCTCCCCCTT CTTACTGATG 120 CAAAGCTCGG CGGAGGCAAG CTTGTCCTGA AACCACTGGG CTTGGCGTTG CCTCACTATT 180 CCGACTCATC GAAAGTCGGC TATGTTCTTG AAGGAAGAGC GGTGGTGGGG CTAACACTCT 240 20 ATGGAGAGAC CGAGCAGAGG ATACTGCTGC TTGAGAAGGG AGATGTGGTA GCGGTGGTCA 300 TGGGGAGCCT CACGTGGTGG TACAACGAGG AGGAGGACTC CGACTTCTCC ATCGCCTTCT 360 -25 TAGGCGATAC CGCGACAGCT GTGCGACCGG GCGACATCGC CTACTTCTTC TTGGCAGGAT 420 CCCTAGGAAG TGCTCCATGG CTTTTCGACG GAAATTCCTC ANCAGGGCCT GCGGTTTAAG m 480 a GGGATGCGGA AGCTGANGAG CTCTTCGGAA GCCAACCTGG TACTCTAATC ATCACACNGC 540 130 AGCAAAAGCT GCCTGGCCTC AGANCATCCC GAGCTGACAG CNAAGGGATA TCNTAAACGC È s b 600 TGANCGCGTA NCGGCATATA TCAATGTGAA AAGTGGTGGC TGTTCTGCCT CGGTGACCCT 660 TNATNAACTG GCNGCNCTGG GAAGATCAGG TTCTCCGTCN ACCTCCAAAA ATCCANCCTA .35 720 N ACCCCGTGCC TTGCCGGGGT TCTTCNTTGA ATCNNCTGTT CANCTGAAAT TTTTCCCCAA 780 fü 40 GGCCNTGGAA CAATTCT 797 (2) INFORMATION FOR SEQ ID NO: 20: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 742 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single 45 (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA 50 (vii) IMMEDIATE SOURCE: (B) CLONE: U-U90 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20: GGCACGAGAT GACTCTCCG GCGGTAGCAT CGGATGCCGA TGATTCGGTC GCTTATACAT 60 60 TCGCTTCGCG ATACGTTCGC GAGGCTCTTC CCCGGTTCAG GATACCGGAG CAGTCGATCC 120 CCAAGGATGC GGCGTACCAG ATCATCAACG ACGAGCTGAT GCTCGACGGG AACCCGCGGT 180 65 TGAATCTGGC GTCGTTCGTG ACGACGTGGA TGGAGCCGGA GTGCGATCGC CTCATCATGG 240 CGGCCGTCAA CAAGAACTAC GTCGACATGG ACGAGTACCC CGTCACCACC GAGCTCCAGA 300

ATCGCTGCGT AAATATGATA GCCCACCTTT TCAATGCCCC AATTGGGGAA NACGAAACGG

CTGTTGGAGT TGGAACTGTG GGTTCCTCCA GAAGCAATCA TGCTTGCAGG ACTTGCATTC

	AAGAGGAAAT GGCAGAACAA AAGAAAGGCA GAGGANAAGC CTTACGACAA ACCCAACNTT	480
5	GTTACCGGTG CAAATGTTCA GGTTTGCTGG GANAAATTTG CAAGGTATTT TGAAGTTTGA	540
3	ACTGAAAGAA ATTGAAGTTG AAAGAAGGAT ATTATGTTAA TGGATCCTGC CAAGGCAGTA	600
	NAAATGGTTG ATGAAAAATA CATATGTTTT TGCTGCCATC TTTGGGTTCA ACTCTCCCTG	660
10	GGAAAATTTG AANATGTTAA CCTTCTAAAT GATCTCCTGA CNGAAAAAAA CCCAGAAACT	720
	GGGTTGGACC CCCCNTACTT GT	742
15	(2) INFORMATION FOR SEQ ID NO: 21:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 807 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
i i	(ii) MOLECULE TYPE: cDNA	
]].		
T 25	(vii) IMMEDIATE SOURCE: (B) CLONE: U-U92	
Stant Stant		
¹ 30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:	
	GGCACGAGCT CTAGCCGATG ACTCTCTCGG CGGTAGCATC TGATGCCGAT GATTCGGTCG	60
]]35	CTTATACATT CGCTTCGCGA TACGTTCGCG AGGCTCTTCC CCGGTTCAGG ATACCGGAGC	120
in the second	AGTCGATCCC CAAGGATGCG GCGTACCANA TCATCAACGA CGAGCTGATG CTCGACGGGA	180
	ACCCGCGGTT GAATCTGGCG TCGTTCGTGA CGACGTGGAT GGAGCCGGAG TGCGATCGCC	240
<u>+</u> 40	TCATCATGGC GGCCGTCAAC AAGAACTACG TCGACATGGA CGAGTACCCC GTCACCACCG	300
	AGCTCCAGAA TCGCTGCGTA AATATGATAG CCCACCTTTT CAATGCCCCG ATTGGGGAAN	360
45	ACNAAACGGC TGTTGGAGTT GGAACTGTGG GGTCCTCAAA AGCAATCATG CTTGCAGGGC	420
	-TTGCATTCAA- GAGGAAATGG -CANAACAAAA- GAAAGGCAGA GGANAAGCCT TACGACAAAC	480
	CCAACATTGT TACCGGTGCA AATGTTCNGG TTTTGCTGGG AANAAATTTG CAAGGTATTT	540
50	TGAAATTTGA ACTGANAGAA NTGAANTTGA AAGAAGGATA TTATGTTTAT GGATCCCNGC	600
	CCAAGGCAGT ANAAATGGTT GATGAAAATA CCAATTTNTG TTGCTTGCCC ATCTTTGGGT	660
55	TCCACTCTCN CTGGGANAAT TTTGAAAAAT GTTNAGCTTC TAAATGATCT CCNGGACCNA	720
	AAAAANNCCC NNAANCTNGG TTGGGACCCC CCCNTACCTT TTCNATNCCT GCCANTTNGG	780
	GGATTCNNTA NCGCCTTTCC TNCTATC	807
60	(2) INFORMATION FOR SEQ ID NO: 22:	
65	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 770 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown 	

(vii) IMMEDIATE SOURCE:

(ii) MOLECULE TYPE: cDNA

(B) CLONE: U-U91

5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:	
	GGCACGAGAG AAAAAATTGT AAAGTTTGAC TTTCATGGAC AGCCTGCGGA GCTCAAGCAT	60
10	GGTAGCCTTG TCATAGCAGC AATTACAAGC TGCACAAACA CATCAAATCC CAATGTTATG	120
	CTTGGTGCTG GTCTTGTTGC AAAGAAGGCC TGTGAATTAG GTCTACAGGT TAAGCCTTGG	180
	ATCAAAACCA GCCTTGCTCC AGGTTCTGGA GTTGTTACCA AGTATTTGCT TAAGAGTGGC	240
15	CTACAAGAAT ATTTGAATCA GCAAGGATTT AATATTGTTG GGTATGGCTG CACAACATGT	300
	ATCGGAAACT CTGGGGATCT TGATGAGTCT GTGGCTGCTG CAATTTCCGA TAATGATATA	360
20	GTTGCTGCTG CTGTTCTATC TGGAAATAGG AATTTTGAGG GACGTGTGCA TCCATTGACA	420
77	CGAGCTAACT ATCTTGCTTC ACCTCCGCTT GTTGTAGCTT ATGCGCTTGC TGGAACAGTT	480
£[]	GACATTGATT TTGAAAAAGA ACCCAATTGG AACAGGGGAA GGATGGGAAA AAACATATAC	540
2 <i>\$</i> []	TTCCAGGATA TATGGCCGTC CACTGAANAA ATTGCACAGG TTGTGCAATC CANTGTTTTT	600
The Control	GCCTGAAATG TTCAAGAATA CCTATGAAGC AATCACCAAA GCACCCTATG TTGGAACCAA	660
30[[]	CTGACTGTTC CCNGCCACAC TCTTTATTCA TGGGACCCAA TCCNCNTACA TCTTAACCAC	720
E E	CNTATTTTAA GGANATGACC ATGGCCCNCC TGTCCNCATG GGGTGAAAAA	770
	(2) INFORMATION FOR SEQ ID NO: 23:	
54D TU	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 810 base pairs	
11)	(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
0[]	(D) TOPOLOGY: unknown	
* ***	(ii) MOLECULE TYPE: cDNA	

(vii) IMMEDIATE SOURCE: (B) CLONE: U-U96

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23: 50 GGCACGAGAG GGCCGTTCCT TTTTGTGCTC GCTTTGCTGC CTCCTCGTTC GTCTTTTCCG 60 CGAATTTCAC CGGCCATGAA CAGCCTTCGG AGCCTTCCGA CATCCTCCGC TCCGCCCTCG 120 55 CCGGTCCCGA GAGGACGTTC GAGTAGGCCA CCGACCTTGA ATCTGGGGGT GATACGACCA 180 CATCATCTTC GTGTAAATGT CGCCAGGAGT GCATGTTCCA AGTCTTCTGC AAGTCCTGAG 240 AAGACTGGTG CTGAAGTGCA AGATCAGAAG TCTGAGATAT ATAGCAGTGA TATGACAAAA 300 60 GCAATGGGTG CAGTGCTGAC ATATAGGCAT GAGCTTGGAA TGAATTATAA TTTCATCTAC 360 CCAGGATTGA TTGTTGGTTC TTGTCTACAG ACCCCATCAG ATGTTGATAA GCTTCCNAAA 420 65 GATTGGGGTT GAAGACCATC TTTTGCTTGC AGAAGGACTC GGATCTTTGA ATATTTTGGG 480 GTTGAAATTG GTGCAATTCC NTGAATATGC CATGCAATGT GGTGACATTG AACATCTTCN 540 TGCTGAAATC AGGGATTTTG ATGCATTTGA TTTGAAGATG ANACTTCCTG CNGTANTTAC 600 70 NAATTATACA AGGCTAATTA ATCCGAATGG TGGAATGACT TATTTTCNCT GTACANCONG 660

	GCTTGGAAAA CGCCTGCANT TGCNTTGGCA TACNTGTTTT TGGGTTNAAG GCTATGAACT	720
•	GAATGAAAGG GCCCCNCTAC TGCNAAATTA NCCAACTTGC TCCCCNAAAT TTGGTGCTAT	780
5	AAAAANTGCC ACCNTTGATA TGCTTATNGG	810
	(2) INFORMATION FOR SEQ ID NO: 24:	•
10	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 765 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	
15	(D) TOPOLOGY: unknown	
	(ii) MOLECULE TYPE: cDNA	
20	(vii) IMMEDIATE SOURCE: (B) CLONE: U-U103	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:	
25	GGCACGAGCT TGGCTGTAGT CTTCTTCTCA AGTAATCTTC GTCTTCCTGA TTTGCTTGGT	60
	TGGTGGTCGG TTGCAGGGCG AAGGGATGGG GATGGGGAGG CCGAGCGGAG CTTGGTCGAC	120
30	CCCGTGGTTG GTGGTGGTTC TTGTGCATTG GCTCCTCTGG GCCACCGAGA GGAGGCGAGG	180
	GGCGGTGGTG GAGGCCTCCC ATGTGGAGTT TGCATCCCTC CAATCTGTTC CTGCCTCCGT	240
26	CGTCGACAAC AGGCTGAGGA CTGGGTATCA CTTCCAGCCC CCGAGGAACT GGATCAACGA	300
35	TCCAAATGGA CCCATGTACT TCAATGGCGT CTACCACCTC TTCTACCAGT ACAACCCCAA	360
	TGGCTCCGTG TGGGGTAACA TCGTGTGGGC CCACTCGGTG TCGACCGACC TCGTCAACTG	420
40	GATAGCACTC GACCCGGCCA TCCGCCCCAG CAAGCCATTC CACATCAACG GATGCTGGTC	480
	CGGCTCCGCC ACCGTCCTCC CCGGCAACAG GCCTGCGATC TTCTACACCG GCATCNACCC	540
45	CCANCANAAA CAACTGCANA ACNTTNCNTN CCCAAGGATC TGTCCAACCT TACTCCCCNA	600
	NTGGGTCAAC CCCACTNCAA CCCCGTGATC CCCCTGGCGA -CGCATCAACN - CCACCCCTTC	660
	CNCNAACCCN AATACGGNTT GGCGCNGTCC CNGCACCCNC TGGAAACCCC TNGTNGGGAA	720
50	CNANTTGAAN CNGAAGGGGA AAGGCNTTCT TTNCCGAACA GGGAT	765
	(2) INFORMATION FOR SEQ ID NO: 25:	
55	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 774 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown 	
60	(ii) MOLECULE TYPE: cDNA	
65	(vii) IMMEDIATE SOURCE: (B) CLONE: U-U93	
	(will engineer description, SEO ID NO. 25.	

GGCACGAGCG GAGAANGCAA TCTCGCTCTC TCTCTACTGC ATCGCGGCTC TCGTCCTCGA



•	TTACTTGAGA TATGGCAGGA AAGGGCGAGG GGCCGGCGAT CGGGATCGAT CTCGGCACCA	120
	CGTACTCGTG CGTCGGGGTG TGGCAGCACG ACCGGTGGA GATCATCGCC AACGATCAGG	180
5	GGAATCGTAC CACCCCTCC TATGTCGCCT TCACCGACTC CGAGCGCCTT ATCGGCGACG	240
	CTGCCAAGAA CCAGGTCGCC ATGAACCCCA TCAACACCGT CTTTGATGCA AAGCGTTTAA	300
10	TTGGTAGGCG ATTCAGTGAT TCATCTGTCC AGAGTGACAT CAAGCTCTGG CCTTTCAAGG	360
	TCATTCCTGG TCCAGGTGAC AAGCCCATGA TTGTTGTCCA ATACAAAGGG GAGGATAAAC	420
	AGTTTGCAGC TGAAGATATT TCTTCCATGG TTTTGATAAA GATGAAAGAA ATTGCTGAAC	480
15	CTACCTGGGG TCTGTTGTCA AGAATGCCGT CCTCACTGTT CCCGCTTACT TCAATGACTC	540
	NCAACGCCCA GCCACAAAGG ATGCTGGTGT CATTGCTGGT CTCNATGTTA ATGANAATCA	600
20	TCAATGANCC CCCAGCACTG CTATTGCTTT ATGGCCTTGA CAAAANGCTA CTATTGTTGG	660
	TGAAAAAAT TTCCTCATCT TCCATCTCCG GTGGGTGGCC TTTTGANTTC NCCTTCCTNA	720
4[]	CCATCCAAGA AGGTTTCTTT NAAGTCAAGG CCCTGCTGGT GANACCCANC TTGG	774
VI25 TI	(2) INFORMATION FOR SEQ ID NO: 26:	
100 mm 10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 786 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
8 8 13 13 15	(ii) MOLECULE TYPE: cDNA	
of the table of table of the table of tabl	(Vii) IMMEDIATE SOURCE: (B) CLONE: U-U125	
:	(xi) SEQUENCE DESCRIPTION: SEQ ID NO. 26.	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

	OGCACGAGCI	MOTOTOGAGI	TITITITI	TITTTTTTAA	AATTGAAATT	AGATGCGATT	60
45	-TEGAATAGCA	-AACATAGTTC-	AGGATAAACC	-AACAACATTG	TACCGAATTC	_GATAAGCTTA	_12.0_
	GGAAACTAAA	TTGCGTAAAC	GAAACACTTG	CATGAAAGCC	TATATAATAT	AAGGCCGACT	180
50	AGGGACNAAA	TAACTTAATC	GACCTCCTCG	ATCTTTGGAC	CAGCGCCGCT	GCCACCAGCA	240
	GGAGGAGCAT	CATCATCCAT	ACCACCAGCC	ATGTCAGCAC	CTGCTCCCTG	GTACATCTTG	300
	GCGATGATGG	GATTGCATAT	GCTCTCCAGC	TCCTTCATCT	TGTCATCGAA	CTCGTCGGCT	360
55	TCTGCCAACT	GGTTGCCATC	GAGCCATTGG	ATGGCCTGCT	CGATCGCATC	CTCCGATCTT	420
	CTTCTTGTCA	GCAGCAGCAA	GCTTGGAGGC	AATCTTGTCG	TCGTTAATGG	TGTTCCTCAT	480
60	GTTGTNAGCA	TANTTTTCCA	GANCATTCTT	CCGATTCCAC	CTTCCTTTTT	ATGCTCCTCC	540
	ATCTTCCTGA	CTTGTTACTT	CTCCGCTTCC	CTGCACCATT	TTCTCAATCT	CCTCCTTGCT	600
	GACCTACCTT	GTCCTTGGTG	AAGGTGATCT	TGTTCTCTGT	CCAGTGGTCT	NTCNTCNGCA	660
65	GAAANATTCC	AGAATACCAT	TGGGGTTCCA	AATGTTNCAA	AACCAAACCC	GGTGGATTCT	720
	TGAAGGAAAC	CCCCCCTAA	GGGCCCCAGG	GTGGGAAATC	CCCCCAAAAA	ACCCCAAAT	780 .
70	TTTCCC						786

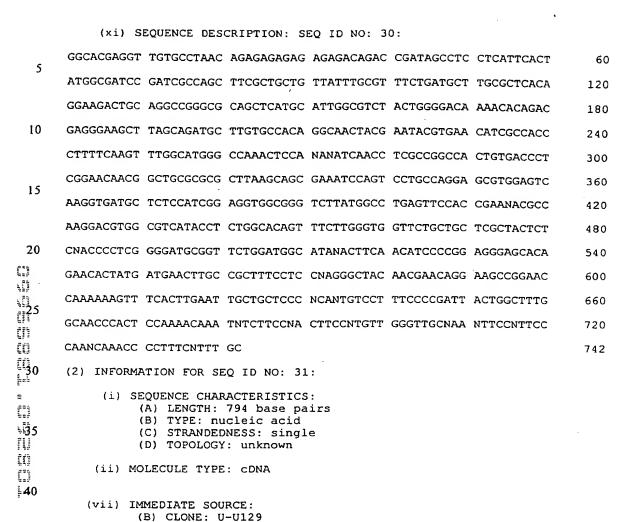
(2) INFORMATION FOR SEQ ID NO: 27:

- 35 -

5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 486 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown 	
	(ii) MOLECULE TYPE: CDNA	
10	(vii) IMMEDIATE SOURCE: (B) CLONE: U-U105	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:	
	GGCACGAGCG AGTTTTTTT TTTTTTTTT TTTTTTTTT TTTTCACAAG GNAACCATAG	60
20	ACATTACACC AAACATAGAT GTCAACAATA CATGCCAACG ATACCATTGC TTATTCCTTC	120
79 79	AGACCTCCGA TAGGACTTCC ACGCACACCA ACAGAGAGAA CTAAGACAGC AAAGCAGCGG	180
id Do	ACACATACAG CCCAAAAGGG TNNGTGACCC CCGCGGAGGN GGAGCNCCAG GTGAAGGGTG	240
11 25 Th	GATTCCCTCT GAATGTTGTA TTCTGNCAGG GTGCGCCCGT CCTCNNTTTG NTTCCCNTCT	300
ij.	NANATCNCCC NCTGNTGATC TGGTGGNAAT CCCCCCCTTG TCCTGTGATT CTTGCTCTTG	360
30	ACNTTTTCT CCCNTGTCNN ANCTCTCTNC CTNCTCTGGG TNTTGGGTCT TCCCCTGTTG	420
i	NANCHNTCTH TTHNCHTATC ATCTTGTNCT CCNNCCNCCN CNCCTNTCNT TTCCTCNNNN	480
135	GGTNNA	486
	(2) INFORMATION FOR SEQ ID NO: 28:	
4.	(:) STOUTHER GUARA CORRESPONDE	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 791 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown 	
45	(A) LENGTH: 791 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	
	(A) LENGTH: 791 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: unknown	
	(A) LENGTH: 791 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA (vii) IMMEDIATE SOURCE:	
45	(A) LENGTH: 791 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA (vii) IMMEDIATE SOURCE:	
45	(A) LENGTH: 791 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA (vii) IMMEDIATE SOURCE: (B) CLONE: U-U116	60
45	(A) LENGTH: 791 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA (vii) IMMEDIATE SOURCE: (B) CLONE: U-U116 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:	60 120
45	(A) LENGTH: 791 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA (vii) IMMEDIATE SOURCE: (B) CLONE: U-U116 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28: GGCACGAGTG ACAATGTCAA GGCCAAGATT CAGGATAAGG AGGGCATTCC CCCCGACCAG	
45	(A) LENGTH: 791 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA (vii) IMMEDIATE SOURCE: (B) CLONE: U-U116 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28: GGCACGAGTG ACAATGTCAA GGCCAAGATT CAGGATAAGG AGGGCATTCC CCCCGACCAG CAGAGGCTCA TCTTTGCCGG CAAGCAGCTC GAGGATGGCC GCACCTTGGC TGATTACAAC	120
45 50 55	(A) LENGTH: 791 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA (vii) IMMEDIATE SOURCE: (B) CLONE: U-U116 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28: GGCACGAGTG ACAATGTCAA GGCCAAGATT CAGGATAAGG AGGGCATTCC CCCCGACCAG CAGAGGCTCA TCTTTGCCGG CAAGCAGCTC GAGGATGGCC GCACCTTGGC TGATTACAAC ATCCAGAAGG AGTCCACCCT CCACCTTGTC CTCCGCCTCC GTGGTGGCAT GCAAATCTTC	120 180
45 50 55	(A) LENGTH: 791 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA (vii) IMMEDIATE SOURCE: (B) CLONE: U-U116 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28: GGCACGAGTG ACAATGTCAA GGCCAAGATT CAGGATAAGG AGGGCATTCC CCCCGACCAG CAGAGGCTCA TCTTTGCCGG CAAGCAGCTC GAGGATGGCC GCACCTTGGC TGATTACAAC ATCCAGAAGG AGTCCACCCT CCACCTTGTC CTCCGCCTCC GTGGTGGCAT GCAAATCTTC GTCAAGACTT TGACTGGGAA GACCATCACC CTTGAGGTGG ANAGCTCGGA CACCATCGAC	120 180 240
45 50 55	(A) LENGTH: 791 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA (vii) IMMEDIATE SOURCE: (B) CLONE: U-U116 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28: GGCACGAGTG ACAATGTCAA GGCCAAGATT CAGGATAAGG AGGGCATTCC CCCCGACCAG CAGAGGCTCA TCTTTGCCGG CAAGCAGCTC GAGGATGGCC GCACCTTGGC TGATTACAAC ATCCAGAAGG AGTCCACCCT CCACCTTGTC CTCCGCCTCC GTGGTGGCAT GCAAATCTTC GTCAAGACTT TGACTGGGAA GACCATCACC CTTGAGGTGG ANAGCTCGGA CACCATCGAC AATGTAAAGG CCAAGATTCA GGACAAGGAG GGTNTTCCCC CGGACCAGCA AAGGCTCATC	120 180 240 300
45 50 55	(A) LENGTH: 791 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA (vii) IMMEDIATE SOURCE: (B) CLONE: U-U116 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28: GGCACGAGTG ACAATGTCAA GGCCAAGATT CAGGATAAGG AGGGCATTCC CCCCGACCAG CAGAGGCTCA TCTTTGCCGG CAAGCAGCTC GAGGATGGCC GCACCTTGGC TGATTACAAC ATCCAGAAGG AGTCCACCCT CCACCTTGTC CTCCGCCTCC GTGGTGGCAT GCAAATCTTC GTCAAGACTT TGACTGGGAA GACCATCACC CTTGAGGTGG ANAGCTCGGA CACCATCGAC AATGTAAAGG CCAAGATTCA GGACAAGGAG GGTNTTCCCC CGGACCAGCA AAGGCTCATC TTTGCCGGCA AGCAGCTTGA GGATGGCCGC ACCCTGGCAG ATTACAACAT TCAGAAGGAG	120 180 240 300 360

	ACACTGGANG AAGGGCGCAC CCTGGCAGAT TNCNACATTC CNAAAGAATC CACCTTCACC	600
	TGGTGCTCCC CCTCCGCCGG GGTCCCTAAC CCTTTTGGGC TGTATGTNTC CCCTGCCTTT	660
5	GCTGTCTTAA TTCNCTCTGT TGGTGTTCGT TGGAAATTCC CTAATCCNGA AGGTTCTTNA	720
	AAAGGAAATN AANCCNNTTG GGTTTTCCCC TTTGGCCTTT TTTTTGTTTG AAAATCCTNT	780
10	GTTTTTGGTG T	791
10	(2) INFORMATION FOR SEQ ID NO: 29:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 814 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
20	(ii) MOLECULE TYPE: cDNA	
1	(vii) IMMEDIATE SOURCE: (B) CLONE: U-U120	
M	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:	
£i)	GGCACNANCC CGCTTCGGTA GCCATTATTG GTGCCCGTAG AGCGAGTGCT GAGATGGCTT	60
(Ú 30 }	TGAGGGCCTT CTTCCCCCTC TGCATCGCTC TCGTGGTGAC GCTCTCACCT CTGTGTGATG	120
e .	CCACTTCGCC TTACTACACC ATCACACCGC CCACCCCCGT GGCCAAGCCG CCTTCAGTTG	180
₩35	AACCACCACC CTACCACGGC CCTCCGACNA CCCACCCTAA GCCACCGAGT CATGGTGGCC	240
	AACCTCCGTC CCACCATCAC CCAACACCAA TCTACGGTGC ACCCCCTCCG CAACACCACC	300
515 513	ACCACCACCA ACACCACCAC CAACCTGCAC CACCAACTCA CGCANAACAC CCTCCGTACT	360
<u></u> 1-40	ACCACATGCC TTCCCCGCCG CCGCATGGCC AGCACCCGTC ACCACCGTCA CATGATTATC	420
	CCGTACCTCC TGCTCACAAG CCCCGAACTC CGCCGCCGGT TTACAAGTCT CCACCACCGA	480
45	NCCACCGTCC TTACCCTCCA TCGACGCCAC CCCACCATCC GAAGCACCCG CCTTCTCAGC	- 54°0° -
	CGAAGCCGTC NTACAAGGCC CGCCACCATN CAAGAACATC CCTGANCACT CTCCACCGCC	600
50	GCGTCACTAT CATTCTCCGT CTTCACCACC ACCACCACCA CCATACAAAA TAATCTCGTT	660
50	TTGCCATCTT CTCCCGTTTG AAAAAAAANN CAANTGTCCT TTTTATTTAA CCNAATCCAN	720
	GGGGTTTTTN TTAANATTTN AANAAANCNA ANTNTTTTCC CCCCCNTNTT GGTTNATGGC	780
55	CTATGGGTTT GTTTCTCTTC TTGGCTTTTC CCGG	814
	(2) INFORMATION FOR SEQ ID NO: 30:	
60	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 742 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
65	(ii) MOLECULE TYPE: cDNA	

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U126



__ (xi) SEQUENCE-DESCRIPTION: SEO ID NO: 31: GGCACGAGGG CGTGGCGGAG ATGGGGAGCT GGCGGGCTCT GTTGCAGCGG CGGCTGCTGT 60 50 TGCTCTCTGC TTTGGCGGTG GCTGTTCGTG TGAAGGCACT CAGCANANAC NATTTCCCCG 120 CCGGCTTCAT TTTTGGCGCA GGCACCTCCG CTTATCAGGT ANAAGGTGCA GCTGCAGAGG 180 GGGGAANAAC ACCCAGCATT TGGGACACGT TTACGCATGC AGGGAGAACT TTCGACCAGA 240 55 GCACCGGAGA CGTAGCAGCT GATCAGTATC ACAAGTACAA GGAAGATGTG AANCTGATGC 300 ATGANATGGG CTTCGATGCT TACAGATTCT CCATCTCCTG GTCCANAGTT ATCCCCAATG 360 60 GTCGAGGGCC TGTGAATCCA CAAGGCTTGC GGTACTACAA CAACCTGATC GATGAGCTCN 420 AAAGATATGG AATCCGAGCC TCATGTCACT CTTTACCACT TCGACCTTCC GCAAGCACTG 480 GAANACGAAT NCGCCGGGCA GCTGAACCCA AAGATCGTAN ANGACTTCAC CGCTTACGCC 540 65 AACGTTTTGC TTCANCNAAT TTGGGGATCN AATCTAGCAC TGGATCNCCC ATCAATGAAC 600 CAACATANAT CCCGTCCTCC GCCACNAATT CCGCATCTTC NCCCCTGGCC CCTGCTCTTT 660 70 ATCCCTTNCG CCTCCAACTG CNCCAAGGGC NACTCCCCCC CATTTTNAAN CCCATNNNNT 720

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	CCNCCCCCC CAATTAACCC NTTCTTGCTC TTCCCCCTTG CCTTCANCCA ACCCGCCCNT	780
	TTTCCNAAAA AANA	794
5	(2) INFORMATION FOR SEQ ID NO: 32:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 799 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
	(ii) MOLECULE TYPE: cDNA	
15	(vii) IMMEDIATE SOURCE: (B) CLONE: U-U130	
20		
[]	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:	
	GGCACGAGCC GGCCTCAGGC ATATGGTGCG GTCGCTACAC GTGTTCAGGC AAGGCCGGGA	60
(1) [1) 25	GCCGGCCAGG ATCATCAGGG AAGCACTGTC GAAGGCGCTG GTGAAGTACT ACCCCTTCGC	120
Post Book	GGGGCGGTTC GTGGACNATC CCGAGGGCGG CGGCGAGGTT CGTGTCGCTT GCACTGGCGA	180
1030	GGGCGCTTGG TTCGTCNAGG CCAAGGCGGA CTGCAGCTTG GAGGACGTGA AGTACCTCGA	240
ř==	TCTCCCGCTC ATGATCCCTG AGGACGCGCT CCTGCCCAAG CCCTGCCCGG GACTGAACCC	300
≖ 4*** 4=#	CCTCGACCTC CCTCTCATGC TGCAGGTGAC ANANTTCGTG GGCGGCGGAT TCGTGGTCGG	360
₩35	CCTCATCTCC GTCCATACCA TCGCCGACGG CCTCGGCGTC NTCCANTTCA TCAACGCCGT	420
# 19. # 19.	CGCCCGAAAT CGCCCGTGGC CTGCCNAANC CCACCGTGGA NCCTGCATGG TCCCGGGANG	480
	TCNTACCCAA CCCACCTAAG CTGCCTCCCG GTGGCCCGCC CGTGTTTCCC CTCCTTCAAN	540
40	CTGCTCCACG CCACCGTCGA ACTATCCCCT GACCACATCC ATCACGTCAA GTCCCCACAC	600
	TTTGGANCTC ACCCGGCCAA CGCTGCTCTA CCTTCCACNT CCCCATCCCC AACCTGTTTG	660
45_	NAATCCCGCA_CGCCCCGCCN_TCNACCTTGG_AACCCAAGGC-NTTTCCAANG-TTTGCAACCC-	7.20
	TTTTTTCCTT TCCTTCCCCC CCCAAAANAA CTTCCCCCCA CCCTTGTTTT TGCNCCCAAG	780
	TTTTTTCCTT CCTTGCCCC	799
50	(2) INFORMATION FOR SEQ ID NO: 33:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 759 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
60	(ii) MOLECULE TYPE: CDNA	
<i>(-</i>	(vii) IMMEDIATE SOURCE: (B) CLONE: U-U43	
65		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:	
70	GGAGGTTGTT GTTCATGTCC CTACTTCGGG GTCTCCTGTA CAGATTGAAT TTCAAGTAAC	60
	TAATAGCAGT GGCTACTTGG TGCTTCATTG GGGTGCAATT CATAATAGAA GGAATAACTG	120

	GTCACTTCCT TCTCGTCATC CTGATGGAAC AAAAGTATAC AAAAACCGAG CTCTCAGGAC	180
5	ACCTTTTAAA AAATCTGGTT CCACATCATC AGTAAAAATG GAGATTGATG ATCCTGAAAT	240
J	ACAAGCAGTT GAGTTTCTCA TATTTGACGA GTCAGAAAAC AAATGGTTTA AACATAATGG	300
	TCAGAATTTC CATGTCCAGT TATTAAAACA GGGCTATCAA AATCAAAATG TTTTGGCCTC	360
10	TGTAAATCCA AATGTTTCAC TGCCANAAAG AACTTGTGCA GATTCAAGCT TATCTTAGGT	420
	GGGANANAAA GGGTAGGCAA ACATATACAC CTGATCAAGA AAAGGATGAG TNTGAAGCAG	480
15	CTANAACTGA GTTTGCTANA AAAACTAAGT NNAAGTACTT CTGTANANGA NCTCCGATCT	540
13	AAATTGACAA AAAACNCCAC TGCTGGAGCG GACAAATCCG TCAAAGTTGA AACTATCAAA	600
	AGTGGGATCC GGATGATCTT NTGCAAGTTA CANGCATACT TCCNATNGGA AAAACCGGGA	660
20	AACCATNTTA TCCCCCNGAA AAACACTNAT GGAATTGAAG AAACCAGGGA AANACTGCCC	720
ffi Laj . Fi	ATGAATTAAA TAAANGAACN CNCCTNCAAA CTNAGGGAA	759
<u>1</u> 25	(2) INFORMATION FOR SEQ ID NO: 34:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 785 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown 	
=	(ii) MOLECULE TYPE: cDNA	
F-1	(wii) IMMEDIAME CONDCE.	
	(vii) IMMEDIATE SOURCE: (B) CLONE: U-U70	
el. El.	(B) CLONE: U-U70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:	60
	(*i) SEQUENCE DESCRIPTION: SEQ ID NO: 34: GGCACGAGAG AGAGAGAGA AGAGAGAGAG AGAGAGAG	60
	(B) CLONE: U-U70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34: GGCACGAGAG AGAGAGAGA AGAGAGAGAG AGAGAGAG	120
11 11 11 140	(XI) SEQUENCE DESCRIPTION: SEQ ID NO: 34: GGCACGAGAG AGAGAGAGA AGAGAGAGAG AGAGAGAG	12C - 180
100 (100 (100 (100 (100 (100 (100 (100	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34: GGCACGAGAG AGAGAGAGA AGAGAGAGAG AGAGAGAG	12G 180 240
11 11 11 140	(XI) SEQUENCE DESCRIPTION: SEQ ID NO: 34: GGCACGAGAG AGAGAGAGA AGAGAGAGAG AGAGAGAG	120 180 240 300
100 (100 (100 (100 (100 (100 (100 (100	(XI) SEQUENCE DESCRIPTION: SEQ ID NO: 34: GGCACGAGAG AGAGAGAGA AGAGAGAGAG AGAGAGAG	120 - 180 - 240 - 300 - 360
100 (100 (100 (100 (100 (100 (100 (100	(XI) SEQUENCE DESCRIPTION: SEQ ID NO: 34: GGCACGAGAG AGAGAGAGA AGAGAGAGAG AGAGAGAG	126 - 180 - 240 - 300 - 360 - 420
45	(XI) SEQUENCE DESCRIPTION: SEQ ID NO: 34: GGCACGAGAG AGAGAGAGA AGAGAGAGAG AGAGAGAG	120 - 180 - 240 - 300 - 360 - 420 - 480
45	(XI) SEQUENCE DESCRIPTION: SEQ ID NO: 34: GGCACGAGAG AGAGAGAGA AGAGAGAGAG AGAGAGAG	120 180 240 300 360 420 480 540
45	(X1) SEQUENCE DESCRIPTION: SEQ ID NO: 34: GGCACGAGAG AGAGAGAGA AGAGAGAGAG AGAGAGAG	120 - 180 - 240 - 300 - 360 - 420 - 480 - 540 - 600
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34: GGCACGAGAG AGAGAGAGA AGAGAGAGAG AGAGAGAG	126 - 180 - 240 300 360 420 480 540 600 660
45	(X1) SEQUENCE DESCRIPTION: SEQ ID NO: 34: GGCACGAGAG AGAGAGAGA AGAGAGAGAG AGAGAGAG	126 - 180 - 240 300 360 420 480 540 600 660 720
45 50 55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34: GGCACGAGAG AGAGAGAGA AGAGAGAGAG AGAGAGAG	120 180 240 300 360 420 480 540 600 660 720 780
45 50 55	(X1) SEQUENCE DESCRIPTION: SEQ ID NO: 34: GGCACGAGAG AGAGAGAGA AGAGAGAGAG AGAGAGAG	126 - 180 - 240 300 360 420 480 540 600 660 720

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PCT/GB97/02424

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5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 784 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
	(ii) MOLECULE TYPE: cDNA	
10	(vii) IMMEDIATE SOURCE: (B) CLONE: U-U16	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:	
	CGGCACGAGG AAANGACNAG CGATGGCAGC AGAATTGTCT CCCACGCTGA GCAAGAGCAT	60
20	CTTTGAAGGA GCCGGTGGAT CTTACTCTAC TTGGTCAGGT GCCGATCTCC CCCTTCTTAC	120
20	TGATGCAAAG CTCGGCGGAG GCAAGCTTGT CCTGAAACCA CTGGGCTTGG CGTTGCCTCA	180
	CTATTCCGAC TCATCGAAAG TCGGCTATGT TCTTGAAGGA AGAGCGGTGG TGGGGCTAAC	240
25	ACTCTATGGA GAGACCGAGC AGAGGATACT GCTGCTTGAG AAGGGAGATG TGGTAGCGGT	300
il il	GGTCATGGGG AGCCTCACGT GGTGGTACAA CGAGGAGGAG GACTCCGACT TCTCCATCGC	360
(() ((30	CTTCTTAGGC GATACCGCGA CAGCTGTGCG ACCGGGCGAC ATCGCCTACT TCTTCTTGGC	420
1430 [-1	AGGATCCCTA GGAGTGCTCC ATGGCTTTTC GACGGAATTC CTCANCAGGG CCTGCGGTAT	480
e 21)	AAGGGATGCG GAANCTGAAG AGCTCTTCGG AAGCCAACCT GGTACTCTAA TCATCNCACT	540
្នា35	GCANCAAAAG CTGCCTGGCC TCANAAGCAT CCCGAGCTTG ACNGCGAAGG GATAGTCNTN	600
	AACNCTNANC GCGTTNCGGC ATATATCAAT GTNAANAGTG GTGGCTGTGC TGCGTCCGTG	660
[]	ACACTINATG AACTGGCCGC GCTGGGAAGA TCTGTTCTCC GTCNAACTCA CCANANTCNA	720
40	ACCTAACCCC NTNCNCTTCC NGGGTTCTCC TTNATGCACT NTGCNCCTAT TTNTTTCCCA	780
	ANGC	784
45	(2) INFORMATION FOR SEQ ID NO: 36:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 817 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
	(ii) MOLECULE TYPE: cDNA	
55	(vii) IMMEDIATE SOURCE: (B) CLONE: U-U30	
60	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:	
	CGGCACGAGA TATGGAGGTA TGATCGGGAG CTACTGGGAG CTCCGCTTTG GTGAACAACA	60
65	CGACGGCAAG AAGGGCTATG GATTCAAGGA GTGAAGGCCA TGGTACCGCA NAGGCGGGTC	120
	TTCCGGGCGT GCACCGAATT TTGCATCGGA TGAAAACCTT GGTCATCAGC ATATGGGGGC	180
	TGGGTTCCAC CAAGGGAAAA GTTCGAATGC AAGTACCAGT GAGTCCCATG AGAGGGACTT	240

GATCATGCAG AGGTATGATC GAAGCAGCTG GAGANTTGGA CTGCTCCANA GCTCATATTC

	GCTTAAGGGA GCCCGACAAG TCAGAGGACA AGGTCGAGTA AGCGAACGTT GCTACCCAAA	360
5	ATCAAGCATC AGTTANAATG GAGGTGGACT CANAGGAGTG CCACGGAAGA CATCTCTACT	420
,	GATTGTGAAG GAAAGGGATA CAGAGGCGAA NCGACGGATA NTANGGCCAT GGGCATGGCA	480
	GCGCCATGGT ACCGCANANG CGGGACTTCC GTGCAAGTCA TTGATCCCTT GCTCTCACGG	540
10	AGGGANANCG CTTGGTCCTG AAAGGGGCCN AAGAAGTGGA CATGCANANG CAATCTCCAA	600
	TTACCGAAAC ANGGCTGAAG GGCANAAGCC NANAAACTTC CTNAGAACGG TGTCAACAAT	660
15	TTCTCATCNA NATANCCGTA ATTAANGACT TCCGGTCATG CNANAATNCC CNACCNANGA	720
13	ACCAANCAGG CNTACTTGTG CTGTNCTTTG CTACCCNNTG AATNGCGCCN GGTTNATNGA	780
	AAAAACGTCC TTCCCCAAGC AACCCTCTNT CAAAAAN	817
20	(2) INFORMATION FOR SEQ ID NO: 37:	
am, am, Q.5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 837 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
	(ii) MOLECULE TYPE: cDNA	
130 130	(vii) IMMEDIATE SOURCE: (B) CLONE: U-U40	
1 5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:	
15 15	TTTTTTTTT TTTTTTTGG GTATCAGGCA AAGATGGATA CTTCCAGGTT TGCTATTTAA	60
40	GAACCATAGT CAGTCTTATG AGGAGAGACC ATACGTAATA CAATCTTTAA GATGACAAAA	120
	TCCATTCCTA CCAATACAAT GACCAAGCGA AAGGTACAAG GATAACGGGC AAAAGACTAA	180
45	ATTGCAACTA TATAAAATTC TGCTGCATTG TAGTAAATTC AACTGTGACG ACACGCCACC	240
	AGGATGAAGT CTATCTATAA ACCCACTTAT TGCTAGATGG ACGGTGTAAC AGAGCTAAAA	300
a	CAGCAAAGTA GAATAAAAGA AACTGACAAC GCTTCCGCAT GCGCTCCACA TATGGAGCCA	360
50	GGCGGAGGTT GGGCAATTGG AGGAAATGAC NTTTCTGACG GTGTAACATA AAANAAATTT	420
	GTAACACCGT CAAGTACGAT TTCCCATCCT TCGGGTTGTG GCGTTCTGCT ACTTGGCATT	480
55	ACGTTAACAT CGAGTGCCGA CTTGGCAAGA CAGGACCCCA GCATCAGAAG TCAGTGTGTC	540
	AACCAAGGAA GAAGGCTTGG CCCCAAAGCT GGAGGCCCGT GCGTAACTGG CTGAACCCCT	600
	GCACCGGAAN GGGTGAAAAA AGCACCATTC AGAACAGGTC NCCTCCGACC TCCCAATTCC	660
60	AGTTCTTCCA CCNTGCTTTT GATCTGTGTC CACCTTTTTG TTACCTATTC CATCGAAGCN	720
	TANGGATTTT TAAAAATCCC GAAGGAAAGG AANTTCCNAT AATTGGTGCN CCAAANAAGG	780
55	AAGATGGACN GAACTGTTGT TGGTTGCTCC TGTTCCTCCT TTGCAATGGA TTGGTCG	837
	(2) INFORMATION FOR SEQ ID NO: 38:	
70	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 799 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	



	(D) 1	OPOLOGY:	unknown
(ii)	MOLECU	LE TYPE:	CDNA

(vii) IMMEDIATE SOURCE: (B) CLONE: U-U108

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:	
GGCACGAGGC AGCTCAATCG ACCGACTCCT CCTCCTCCTC CTCCTCCTCC TCTTGTTCT	r 60
CTCATTCTAA TATAATTATC GCTTTTGGTG TGTACATCTT CTATAATTTG AGAGGATGG	120
GGCAGGATTG ATGGCGAAAC AAGCAGCAGC GGTTGCGAAG CCGAACGCGT TCCCCGCCCC	180
GAGCCTAGGG TTCGGGAGCT CGGTCAGGGG CGGATCCGGG ACCAGCAGGA TCGGGTTCGA	240
GGCGCCCGCG AGCGTGGCAT GGAGGAAGCG GTCGATTCAG GTGGCCCGCC AAGGAGCCAT	300
TCGGTCGGAG GTGGTCGTGG AANANAAAGC ATCNCCGCCC AAAAAGGATA AGGCCGGTCG	360
GGGTCGGCTC TACGTGGGTC TGCCCTTGGA CGTGGTCTCC GACGGCAACG TCNTCAACCA	420
CGGCAAGGCC ATCGCCGCCG GTCTCCGCGC CCTCCGCCCT CCTCGGCGTT GATGGANTCN	480
AACTCCCCCA TCTCCTGGGG CGTTGGCGAT GGACTCCGGC GAATGGTCCT CCTACCTCCC	540
CCGTCNCCGC CATGGCGCGC GACNCCCGGC CTTCGCCTCC GCGTCTCCCT CCACCTCCAC	600
TGCCANCGCC GCCCTCGCCT CCCCCTCCCC NAATCGGTCG AATCCNCCGC CGCTAACAAA	660
CCCCGAAATC CTATTCNCTG AACGCNCCGG CCGCCNCCNG TTGCCCAAAN TNGCCTTNTT	720
CCTTTCCNCT TTGTTTNAAA AAAAACTCCC CNTTGTTCCT TCCAANCGGG NAGGAACCCC	780
CNAATGGAAA CCTTNCAAA	799

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 786 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single---(D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE: (B) CLONE: U-U128

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

60	GGCACGAGGA	AACGTCTCTC	CCTCTCTCCA	CTTCTCACAC	CCCCCCCCC	GACTCAGCGA	60
00	ATCGACATTC	TTGGCGTGTC	AAGGAAACCT	TTCTTTTATT	TGCGAAGGAA	CATGAGCAAT	120
	ACTGTTGGAC	ACACCTTACC	CCAGCAAGCT	CTTTACCGGC	CTTCTATCAA	AGAAAATCAA	180
65	AGTAAAGCTC	ATCAAGGAGT	TTCTGCAAAC	TTCTTGTGTG	GAGTTCCATT	AGGATCTAAG	240
	GTGGAAAATG	CAGTGTCATA	CAGCTCTAGG	TCACTGCTTT	CAACCGGATC	CCTGGGAAAG	300
70	AAACTCATCA	AAGGAATCCC	ACCAAAGCAA	AATCCAAGCA	TAGTCACTAT	GACCCCTCGT	360
	GCTGTGTTGG	CTGCANATCC	TGCTTCAGAG	CTAAGGAGAA	AATTCAAGCT	TGACACAAAT	420

	TCTGAATTGG AGGTTGTTGT TCATGTCCCT ACTTCGGGGT CTCCTGTNCA GATTGAATTT	480
5	CAAGTNACTA ACAGCAGTGG CTACTTGGTG CTTCNTTGGG GTGCAATTCA TAATANAAGG	540
,	AATAACTGGT CACTTCCTTC TCGTCATCCT GATGGAACAA AAGTTTNCCN AAACCCGAAC	600
	TCTCANGANA CCTTTTAAAA AATCTGGTTC CCCATCNTCC GTNAAAATGG AGATTGATGA	660
10	TCCTGAAATA CCAGCAGTNG AATTTCTCCT TANTTTTGNA ACAAATNCTC AAAAAAACCN	720
	AAATTGGGTT TTTAAAACNA TTAATGGGTC CCNAAATTTC CNTGTTCCNN TTTTTTTANA	780
15	AACAAG	786
.,	(2) INFORMATION FOR SEQ ID NO: 40:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 804 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
125 1125	(ii) MOLECULE TYPE: cDNA	
11 11 130	(vii) IMMEDIATE SOURCE: (B) CLONE: U-D4	
ļab -	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:	
2 - 1 2 - 1 3 - 1	GGCACGAGAG ATAGCTGAAG TGACGTGAGG TGACTTCGAT TAGATCGAGA GAAATTTCTT	60
្រូ <u>3</u> 5 ការ	TGTGATTTTT GTGGACAATT CTCAATGGCT GCTGTAACAA ANTCACAATT CATCTCGAAA	120
	GGCTCATGCG CTGGCTATGG GGGTGTCGTC GACTCGGAGC CAAGGACCTT CCTAAACAGA	180
[1] [4]0	AGGGTTCTAC ACTTGAGGAA CCAAACCACC GCTTACGAAG GATTGAGATC TCGAAATGTG	240
	GTTGATTTGA TTCAGATGCC GTCTAATGCC AAGGTGATTT CAAGGAAAAC TGTGAGGGGA	300
45	ACTCAGAATC CTAGTCGTAN ACCTTGGGCT GTTGTCATTT GTGGAAAAGG GATGAACATA	360
	GTCTTTGTCG GCGCTGANAT GGCTCCCTGG AGTAAAACCG GANGGACTCG GTGATGTTCT	420
	TGGAGGACTG CCACCGGCCA TGGCTGCAAA TGGACACAGA NTGATGACTA TAGCTCCACC	480
50	CTATGATCAG TACAAGGATG GGTGGGATAC AAATGTCCTG GCTGAATTAA AAGTTGGAAA	540
	TGAAATTGAA ANAATCCGCT TTCTTCCACT GCTATAAAAA AAGAATTGAC AGGGTTTTCA	600
55	TTGATCACCT TTGTTTCTTG AAAANGTGTT GGGAAAAACT GGAAGAATGA AATTTTGGTC	660
	CTNTCCCCGG AACTGATTTT NAAAAACANC CCCTAAANTT TANCCTTTTN TNCCCNGCCN	720
	CTTTTGGAAA CTCCCNGGAT NCTGGTTTTT TNCCACCCCC NAAAANTTTC CTNGAACCTN	780
60	TGGGGGAAAN TTTTTTTTT TTTT	804
	(2) INFORMATION FOR SEQ ID NO: 41:	
65	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 826 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown 	
70	(ii) MOLECULE TYPE: cDNA	

(vii) IMMEDIATE SOURCE: (B) CLONE: U-D10

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41: GGCACGAGAG ATAGCTGAAG TGACGTGAGT GGACAATTCT CAATGGCTGC TGTAACAAAG

60 10 TCACAATTCA TCTCGAAAGG CTCATGCGCT GGCTATGGGG GTGTCGTCGA CTCTGAGCCA 120 AGGACCTTCC TAAACAGAAG GGTTCTACAC TTGAGGAACC AAACCACCGC TTACGAAGGA 180 15 TTGAGATCTC GAAATGTGGT TGATTTGATT CAGATGCCGT CTAATGCCAA GGTGATTTCG 240 AGGAAAACTG TGAGGGGAAC TCAGAATCCT AGTCGTANAC CTTGGGCTGT TGTCATTTGT 300 GGAAAAGGGA TGAACATAGT CTTTGTCGGC GCTGANATGG CTCCCTGGAG TAAAACCGGA 360 20 GGACTCGGTG ATGTTCTTGG AGGACTGCCA CCGGCCATGG CTGCAAATGG ACACAGAAGT 420 Arra denta GATGACTATA GCTCCACGCT ATGATCAGTA CAAGGATGGG TGGGATACAA ATGTCCTGGC 480 W 25 TGANTTAAAA GTTGGAAATG AAATTGAAAG AATCCGCTTC TTCCACTGCT ATNAAANAAG 540 m AATTGACAGG GTTTTCATTG ATCATCCTTT GTTTTCTTGA AAANGTGTTG GGAAAAACTG 600 f() GANGAATGAT ATNTGGTCCT GTCCCNGGAA CGGATTATTN AAAACCACCC NCTTAANATT 660 [[] 30 į... TACCCTTTTG TGCCCANGCA NCNTTTGGAA NCTCCCAAGG ATTCTGGATN TTTAACNACN 720 NCCNAATACT TTTCCTGGAA CCATTTNGGG GANAANNTTG TTNTTTGTTG CNAATTAATT 780 **35** GGCNCCCTGG TCCTCCTNCC TGCTACTTAA AAATTTTNTT TCNTNT 826 fIJ (2) INFORMATION FOR SEQ ID NO: 42: Û

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA 45

(vii) IMMEDIATE SOURCE:

(B) CLONE: U-D13

50

<u>|</u> 40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

55 GGCACGAGCT GAGGGAGTGA GGGAAAGAGA TAGCTGAAGT GACGTGAGGT GACTTCGATT 60 AGATCGAGAG AAATTTCTTT GTGATTTTTG TGGACAATTC TCAATGGCTG CTGTAACAAA 120 GTCACAATTC ATCTCGAAAG GCTCATGCGC TGGCTATGGG GGTGTCGTCG ACTCGGAGCC 180 60 AAGGACCTTC CTAAACAGAA GGGTTCTACA CTTGAGGAAC CAAACCACCG CTTACGAAGG 240 ATTGAGATCT CGAAATGTGG TTGATTTGAT TCAGATGCCG TCTAATGCCA AGGTGATTTC 300 65 AAGGGAAAAC TGTGAGGGGA ACTCAGAATC CTAGTCGTAG ACCTTGGGCT GTTGTCATTT 360 GTGGAAAAGG GATGAACATA GTCTTTGTCG GCGCTGANAT GGCTCCCTGG GAGTAAAACC 420 GGAGGACTCG GTGATGTTCT TGGAGGACTG CCACCGGGCC ATGGCTGCAA ATGGACACAG 480 70 AAGTGATGAC TATAGCTCCA CGCTATGATC AGTACAAGGA TGGGTGGGAT NCAAATGTCC 540

	TGGCTGAATT AAAAGTTGGG AAATGAANTT GAAAGAATCC GCTTCTTCCA CTGCTATAAA	600
5	ANAAGAATTG ACAGGGTTTT CATTGATCAC CTTTGTTCTT GAAAAGGTGT GGGGAAAAAC	660
,	TGGAAGAATG ATATTTGGTC CTGTCCCNGG ACTGATTTNA AAACACCACC TAAAATTACC	720
	TTTTGTNCCN GCNNCTTTGG AACCNCCCNG GATCTNGATN TTANCACCCC CAANTCTTAT	780
10	CCTGGAACTT TTGGGGNAAA NTTTGTNTTT GTT	813
	(2) INFORMATION FOR SEQ ID NO: 43:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 805 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
20	(ii) MOLECULE TYPE: cDNA	
	(vii) IMMEDIATE SOURCE: (B) CLONE: U-D66	
11	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:	
() () 30	GGCACGAGAA GAGATAGCTG AAGTGACGTG AGTGGACAAT TCTCAATGGC TGCTGTAACA	60
:3 ¹ 2	AAGTCACAAT TCATCTCGAA AGGCTCATGC GCTGGCTATG GGGGTGTCGT CGACTCGGAG	120
	CCAAGGACCT TCCTAAACAG AAGGGTTCTA CACTTGAGGA ACCANACCAC CGCTTACGAA	180
]35 []	GGATTGANAT CTCGAAATGT GGTTGATTTG ATTCAGATGC CGTCTAATGC CAAGGTGATT	240
12 13	TCAAGGAAAA CTGTGAGGGG AACTCACAAT CCTAGTCGTA NACCTTGGGC TGTTGTCATT	300
40	TGTGGAAAAG GGATGAACAT AGTCTTTGTC GGCGCTGAGA TGGCTCCCTG GANTAAAACC	360
	GGAGGACTCG GTGATGTTCT TGGAGGACTG CCACCGGCCA TGGCTGCAAA TGGACACACA	420
-45	GTGATGACTA TAGCTCCACG CTATGATCAG TACAAGGATG GGTGGGATAC AAATGTCCTG	480
-43	GCTGANTTAA AANTTGGAAA TGAAATTGAA AAGANTCCGC TTCTTCCACT GCTATAAAAN	540
	AAGAATTGAC AGGGTTTTCA TTGATCATCC TTTGTTTCTT GAAAAAGTGT GGGGAAAAAC	600
50	TGGGAAGAAT GATATNTGGT CCTGTCCCNG GAACTGATTA TAAAACACCA GCTAANATTA	660
	CCTTTTGTTG CCAGCAACTT TGGAACCCCN AGGATTCTGG ATNTTACAAC ACNAATACTA	720
55	TTCTGGAACA TTTGGGGAAA AATTGTTTTT GTTNCCAATG ANTGGCNCAC TGGTCCCNTC	780
	CCTNCCTACT TAAAAANTTT TTTCC	805
	(2) INFORMATION FOR SEQ ID NO: 44:	
60	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 790 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
0,5	(ii) MOLECULE TYPE: cDNA	
70	(vii) IMMEDIATE SOURCE: (B) CLONE: U-D111	

	(XI) SEQUENCE DESCRIPTION: SEQ ID NO: 44:	
5	GGCACGAGAA GAGATAGCTG AAGTGACGTG AGTGGACAAT TCTCAATGGC TGCTGTAACA	60
	AAGTCACAAT TCATCTCGAA AGGCTCATGC GCTGGCTATG GGGGTGTCGT CGACTCTGAG	120
10	CCAAGGACCT TCCTAAACAG AAGGGTTCTA CACTTGAGGA ACCAAACCAC CGCTTACGAA	180
••	GGATTGAGAT CTCGAAATGT GGTTGATTTG ATTCAGATGC CGTCTAATGC CAAGGTGATT	240
	TCGAGGAAAA CTGTGAGGGG AACTCAGAAT CCTAGTCGTA GACCTTGGGC TGTTGTCATT	300
15	TGTGGAAAAG GGATGAACAT AGTCTTTGTC GGCGCTGANA TGGCTCCCTG GAGTAAAACC	360
	GGAGGACTCG GTGATGTTCT TGGAGGACTG CCACCGGCCA TGGCTGCAAA TGGACACAGA	420
20	GTGATGACTA TAGCTCCACG CTATGATCAG TACAAGGATG GGTGGGATAC AAATGTCCTG	480
C)	GCTGAGTTAA AAGTTGGAAA TGAAATTGAA AGANTCCGCT TCTTCCACTG CTATAAAAGA	540
#1.5 #1.5	AGANTTGACA GGGTTTTCAT TGATCATCCT TTGTTTCTTG ANAAGGTGTG GGGAAAAACT	600
1 25 1 25	GGAAGAATGA TATATGGTCC CTGTCNCAGG AACNGATTAT GAANACAACC AGCTAAGATT	660
T 11	AACCTTTTGT TGCCAGCACT TTGGGAACCN CAAGGATCCT GGATCTTAAC AACNCAANTC	720
10 10 30	TATTCTGGAC CATATGGGGA CAAATTGTTT TGTTGCAAAT GATGGCACCT GGTCCNNTCC	780
ļ.k	ATGCTACTTA	790
z C)	(2) INFORMATION FOR SEQ ID NO: 45:	
35 [] [] [] []	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 813 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA	

(xi)	SEQUENCE	DESCRIPTION:	SEO	ID	NO:	4.5:	

50	(X1) S	EQUENCE DES	CRIPTION: S	EQ ID NO: 4	5:		
50	TTTTTTTTT	TTTTTTTTTG	GAGCATAATA	GCAATTTATT	CAGGAGGATC	AAACTCAAAC	60
	ACTATAACAT	AGACAGTAGT	CACTTTCAGG	GAGTGGCCAC	ATTTTCCTTT	GCAAGAGGAG	120
55	CTATTTCATC	AGCATCGATG	CCGGCTTCAC	TACCAGCAGC	TCCTAAGCTT	AGGANAAATT	180
	GCTCCCACTT	CTTAGCAGGT	CCCTTCCAGG	AGAGGTCTTG	AGTCATGCAG	TTCTGTATCA	240
60	TCTCAGCAAA	TGCAGGTGTG	CCGTAAACTT	TAAGGGCCCT	TTTCACTGTC	TGAATGACTT	300
00	TTTGTACATC	ATCTTTATCG	ACAACATCAC	AATCAGGATT	GAAGGGACCC	ATATGAAACC	360
	CTGTGATGCC	TTCTATGACA	GTGTCAGCAA	GTCCACCAGT	TGTTGCGCAC	ATGGGGGGAA	420
65	TTCCATATCG	CATGCCCTGA	AAGCTGGATA	AGGCCACAAG	GTTCGAATCT	GCTGGTAAGA	480
	NCAAGAAGAT	CTGCTCCAGC	CATGATTTCA	TGANCCAAAG	GTGCATTAAA	CTTCATATGT	540
70	GCTCTCACTT	TATTGGGAAA	CATATCTTCA	AGTTGTGCAA	GCTGACGCTC	CAACANCTTC	600
, 0	TCCCANTACC	AAGCACTATC	ACTTGAACAT	TTTCATCAAT	GAATTCAGGA	ATAACTGCNG	660

	CGAAAATATC CGAACCTTTC TGCTCTCTAA TCTCCCTATA AAGGNTATAA CAGGGATTTC	72
	CNGTCAACAG GTTAACCAAA TTCAACTTGT TAGGNTTCCC TTAATCCAAA GGTTTGCACC	786
	CNNCCCATTT GTTGCTCNTA ATTGANAAAA ATT	813
	(2) INFORMATION FOR SEQ ID NO: 46:	
1	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 808 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
1	(ii) MOLECULE TYPE: cDNA	
2	(vii) IMMEDIATE SOURCE:) (B) CLONE: U-D39	
[] [] [] 2	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:	
(II	GGCACGAGCG AGTTTTTTT TTTTTTTTT GCTGTGATGA TATTATGCAT CTTATTAGTT	60
	GGTTGCACCA CTTCTATTAC ATCACTCAAC AGTATTAGCC CAAGANAAGG CTAATACCTT	120
[[] 3	CNCATCACTC TTGACATCTT ATTTGTATTG TAGGANACTA GTATATATAT CTATATGCGT	180
He is	GGTTGCCTGC ACNAGGGCGG CTTATTAGTG GCGTCAGTGA TCTCAAGGGC AGAANACAAC	240
[] [] 3:	CCTGTANTTG GTGCCGCCGG GGCAGGTGAA GGTGCTCGTC TGATCGTCCT TGGGATANCT	300
î.	GTAGGCGTCG GGGCAGTTTC TCTTGAANAA CCGGGAGTAT TCGGTCGGGC TGCAGCTGCC	360
	GGAGTTGCAA CAGTACTGGT CCGTCTTGAA CACGGTGCAG GGGTTGTTGC ANCCGCCCGG	420
[] 4(CGCCTTCANC GCCCCGGGC ACTGCCCGTT GATNTCCGCC GCGCACCGGA TGCCGCGGCA	480
	NCCGCCTGAC NTGGGGCTNA ATCCCATTGG CACGTTGAAA CCGTCNACCA AGGGAAATTT	540
45	CAAAAAATCC AAGTTGTTGA ACTGGTTGAA CGCCAACTCC NCCAGGGTNT TGGGCCGGTT	600
	GECNTACCEC GTGCATNACA ACACCCCGCC GCANTCCCCT TCTGGCACCG CCGCNTCCGC	660
	TCCCCTCAAA AGAACACCCG TGCGGCCCAA AATCCGGNCC CCCGGTGGTT CCCCCTTTCN	720
50	CTTTAANGGT CCCCAATGCC CCTGNTTTAA CTGNCTCCCC CCCANGCNCG GCCCCGGCCC	780
	ACNCTTTNTT AAAACATCNG TNCCNAAT	808
55	(2) INFORMATION FOR SEQ ID NO: 47:	
60	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 809 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	
00	(D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA	
65	(vii) IMMEDIATE SOURCE: (B) CLONE: U-D50	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

	GGCACGAGTG TGCCTAACAG AGAAAGAGAG ACCGATAGCC TCCTCATTCA CTATGGCGAT	60
	CCGATCGCCA GCTTCGCTGC TGTTATTTGC GTTTCTGATG CTTGCGCTCA CAGGAAGACT	120
5	GCAGGCCGGG CGCAGCTCGT GCATTGGCGT CTACTGGGGA CAAAACACAG ACGAGGGAAG	180
	CTTAGCAGAT GCTTGTGCCA CAGGCAACTA CGAATACGTG AACATCGCCA CCCTTTTCAA	240
10	GTTTGGCATG GGCCAAACTC CANAGATCAA CCTCGCCGGC CACTGTGACC CTCGGAACAA	300
10	CGGCTGCGCG CGCTTAAGCA GAGAAATCCA GTCCTGCCAG GAGCGTGGAG TCACGGTGAT	360
	GCTCTCCATC GGAGGTGGCG GGTCTTATGG CCTGAGTTCC ACCGAAGACG CCAAGGACGT	420
15	GGCGTCATAC CTCTGGCACA GTTTCTTGGG TGGTTCTGCT GCTCGCTACT CTCGACCCCT	480
	CGGGGATGCG GTTCTGGATG GCATANACTT CAACATCNCC GGAGGGAGCA CAGAACACTA	540
20	TGATGAACTT GCCGCTTTCC TCAAGGGCTA CNACGAACAG GAAGCCGGAA CGAAAAAANT	600
	TTTACTTGAA TGCTGCTCCC NCANTGTCCT TTCCCGGATT ACTGGCTTGG CACCCACTCA	660
75. 75. 75. 75. 75. 75. 75. 75. 75. 75.	NAAAANATCT CTTCCNACTT CCNTGTGGGT TGCANTTCCT CCAANAACCC TTCCTTGCCN	720
10 25 10	TTTCTCCCCA AAACCTATCC ATCTTGCAAT TCCTTTCACA AATTGGGTCN TNTCCNTCCC	780
41 1	NGCCCCNAAA ACTTTTCCC TNGGGCTCC	809
[[] [[] 30	(2) INFORMATION FOR SEQ ID NO: 48:	
ļ-k	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 809 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
្រ្យ 35	(D) TOPOLOGY: unknown	
Harry grang	(ii) MOLECULE TYPE: cDNA	
40	(vii) IMMEDIATE SOURCE: (B) CLONE: U-D86	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:	
	GGCACGAGCC ACAAGCTTGC CTTTGGTTGT GCCTAACAGA GAGAGAGAGA GAGACAGACC	60
50	GATAGCCTCC TCATTCACTA TGGCGATCCG ATCGCCAGCT TCGCTGCTGT TATTTGCGTT	120
30	TCTGATGCTT GCGCTCACAG GAAGACTGCA GGCCCGGCGC AACTCATGCA TTGGCGTCTA	180

CTGGGGACAA AAGACAGACG AGGGAAGCTT AGCAGATGCT TGTGCCACAG GCAACTACGA 240 55 ATACGTGAAC ATCGCCACCC TTTTCAAGTT TGGCATGGGC CAAACTCCAG AGATCAACCT 300 CGCTAGCCAC TGTGACCCTC AGAACAACGG CTGCGCGCGC TTAAGCAGCG AAATCCAGTC 360 CTGCCAGGAG CGTGGAGTCA AGGTGATGCT CTCCATCGGA GGTGGCGGGT CTTATGGCCT 420 60 GAGTTCCACC GAAGACGCCA AGGACGTGGC GTCATACCTC TGGCACAGTT TCTTGGGTGG 480 TTCTGCTGCT CGCTACTCTC GACCCCTCGG GGATGCGGTT CTGGATGGCA TAAACTTCAA 540 65 CATCNCCGGA GGGAGCACAG AACACTATGA TGAACTTGCC GCTTTCCTCA AGGGCTACAA 600 CGANCAGGAA GCCGGAACGA AAAAAGTTCA CTTGAATGCT GCTCCCCANT GTCTTTCCCG 660 GATTACTGGC TTGGCAACGC NCTCCAAAAC AAATCTCTTC CACTTCCTGT GGGTGCANTC 720 70 CTCCACAAAC CTTCNTGCAT TCTCCCCAAA CCTATCAATC TTGCNAAATG CGTTCAACAA 780



		INGGGICIT TICATCCCCG CCCAAAACT	809
	5	(2) INFORMATION FOR SEQ ID NO: 49:	
		(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 785 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	
	10	(D) TOPOLOGY: unknown	
		(ii) MOLECULE TYPE: cDNA	
	15	(vii) IMMEDIATE SOURCE: (B) CLONE: U-D90	
	20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:	
1 .]		GGCACGAGGA GAGACCGATA GCCTCCTCAT TCACTATGGC GATCCGATCG CCAGCTTCGC	60
453		TGCTGTTATT TGCGTTTCTG ATGCTTGCGC TCACAGGAAG ACTGCAGGCC GGGCGCAGCT	120
411	25	CGTGCATTGG CGTCTACTGG GGACAAAACA CAGACGAGGG AAGCTTAGCA GATGCTTGTG	180
age that their think		CCACAGGCAA CTACGAATAC GTGAACATCG CCACCCTTTT CAAGTTTGGC ATGGGCCAAA	240
(1)	30	CTCCAGAGAT CAACCTCGCC GGCCACTGTG ACCCTCGGAA CAACGGCTGC GCGCGCTTAA	300
ř=h m		GCAGAGAAAT CCAGTCCTGC CAGGAGCGTG GAGTCACGGT GATGCTCTCC ATCGGAGGTG	360
13	35	GCGGGTCTTA TGGCCTGAGT TCCACCGAAG ACGCCAAGGA CGTGGCGTCA TACCTCTGGC	420
And and		ACAGTTTCTT GGGTGGTTCT GCTGCTCGCT ACTCTCGACC CCTCGGGGAT GCGGTTCTGG	480
Ü		ATGGCATANA CTTCAACATC GCCGGAGGGA GCACAGAACA CTATGATGAA CTTGCCGCTT	540
11	40	TCCTCAAGGC CTACAACGAG CAGGAAGCCG GAACGAAAAA AGTTTACTTG AATTGCTGCT	600
		CCGCANTATC CTTTCCNGAT TACTGGCTTG GCAACNCNCT CCAAAAAANA TCTCTTCCAC	660
	45	TTCCTGTTGG GTGCAGTTCT TCCAANAACC CNTTCNTGCC ATTTCTCCCC AAAACGCTTT	720
_		CCATCTTTGC AAATGCCTTT CAACAATTGG GGTCTTGTTC CNNCCCTGCC CCAAAAACTG	780
		TTCCT	785
	50	(2) INFORMATION FOR SEQ ID NO: 50:	
	55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 813 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
		(ii) MOLECULE TYPE: cDNA	`
	60	(vii) IMMEDIATE SOURCE: (B) CLONE: U-D93	
	65		
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:	
	70	GGCACGAGCG ATAGCCTCCT CATTCACTAT GGCGATCCGA TCGCCAACTT CGCTGCTGTT	60
	70	ATTTGCGTTC CTGATGCTTG CGCTCACGGG AAGACTGCAG GCCCGGCCCA GCTCATGCAT	120

		TGGCGTCTAC TGGGGACAAA ACACCGACGA GGGAAGCTTA GCAGATGCTT GTGCCACAGG	180
•		CAACTACGAT TACGTGAACA TCGCCACCCT TTTCAAGTTT GGCATGGGCC AAACTCCAGA	240
	5	GATCAACCTC GCCGGCCACT GTGACCCTCG GAACAACGGC TGCGCGCGCT TGAGCAGCGA	300
		AATCCAGTCC TGCCAGGAGC GTGGCGTCAA GGTGATGCTC TCCATCGGAG GTGGCGGGTC	360
	10	TTATGGCCTG AGTTCCACCG AAGACGCCAA GGGAAGTAGC GTCATACCTC TGGCACAGTT	420
	10	TCTTGGGTGG TTCTGCTGCT CGCTACTCGA GACCCCTCGG GGATGCGGAA CTGGATGGCA	480
		TANACTTCAA CATCGCCGGA GGGAGAACAG AACACTATGA TGAACTTGCC GCTTTCCTCA	540
	15	AGGCCTACAA CGANCAGGAA GCCGGAACNA AAAAAGTTCA CTTGAATTGC TGCTCCGCAG	600
		TGTCCTTTCC CGGATTACTG GCTTGGCAAC GCACTCAGAA CANATCTCTT CNACTTCCTG	660
	20	TGGGTGCAAT TTCCTCCACA ANCCTTCCNT GCCATTTCTC CCAAAAAGCT ATCNATCTTG	720
C)		CAAATGCGTT CNACAATTGG GTCTTTTCCA NCCTGCNCAA AACTGTTCCT TGGGCTCCCG	780
4[]		CTGCCCCTGA AGGTGCNCCA ATTGGTGGCT NCT	813
44	25	(2) INFORMATION FOR SEQ ID NO: 51:	
Head that their adh	30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 819 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown 	
£.		(ii) MOLECULE TYPE: cDNA	
der serial de se	35	(vii) IMMEDIATE SOURCE: (B) CLONE: U-D61	
11	40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:	
		GGCACTCAGG AACTCCAACA TCCAAGTCCT GTTGGATGTC CCCCGATCCG ACGTGCAGTC	60
	45	ACTGGCCTCC AATCCTTCGG CCGCCGGCGA CTGGATCCGG AGGAACGTCG TCGCCTACTG	1.20
		GCCCAGCGTC TCCTTTCGAT ACATAGCTGT CGGAAACGAG CTGATCCCCG GATCGGATCT	180
	50	GGCGCAGTAC ATCCTCCCCG CCATGCGCAA CATCTACAAT GCTTTGTCCT CGGCTGGCCT	240
		GCAAAACCAG ATCAAGGTCT CGACCGCGGT CGACACGGGC GTCCTCGGCA CGTCCTACCC	300
		TCCCTCCGCC GGCGCCTTCT CCTCCGCCGC CCAGGCGTAC CTGAGCCCCA TCGTGCAGTT	360
	55	CTTGGCGAGT AACGGAGCGC CGCTCCTGGT CAATGTGTAC CCTTATTTTA GCTACACCGG	420
		CAACCCGGGA CAGATCTCGC TGCCCTACGC CCTGTTCACG GCCTCCGGCG TCGTCGTGCA	480
(60	GGATGGGCGA TTCANCTATC AGAACCTGTT CGACGCCATC GTCGACGCGG TCTTCGCGGC	540
		GCCTGGAAAA AATGGGAAGG GCGAACGTGG CGGTGGTGGT GTCCGAAAAC GGGTGGCCGT	600
		CCGCGGGCGG AAGAACCCNA AACNAACACC ANCAACNCCG CCGGAANTTT CAACCANAAC	660
6	55	TTGATCAGGC ATGTTNGGCG GAAGAACCCC AAGGAAAACC AGGGAAGGAA ATCAAGGCTT	720
		CNTNTTCCAA AANTTTCCAC CAAAAACCNA AAGGTGGANG GATCCAACAA AACTTTGGCC	780
7	70	TGTTTTATCC CAANNAACAN CCCNTCTTAC CNAATAACT	819
,	-	(2) INFORMATION FOR SEQ ID NO: 52:	

5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 794 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown 	
	(ii) MOLECULE TYPE: cDNA	
10	(vii) IMMEDIATE SOURCE: (B) CLONE: U-D63	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:	
	GGCACGAGGG ATTATAAAAA GAAACTCGCA CTCAGCCAGA TTGACTCAAG CATGAAGGTT	6
20	GCATCTTTCG AATGTTCCTT TTTTTTCCAA CATCTTTTGA ATGTTACATG ACAATCATGA	12
: <u> </u>	CGCCGTGCAT ACAATGATAC CTCTGATAGG GTTGAATGCA CAAACCACTC ATCGTGCTAT	18
2 5	ATTGCAAGTG CTTATGTTTG TATTCATTTT CTTATAATTT CAATGTGAGA GTTACCTTAG	24
n	GTTCATATTA NATTTATATA ATATTGGGCA TAGATTTTTT TGTCATTGTT TGTGATCTGC	30
	AATTTCATTA GGTCATCGAC CATATTATGG TAAATTTAAT TTACTAAATT ATATCTTGAG	36
()30	TTTATTGCTT TGCATATTTT GTGCTGGAAA CCATGCCAAT CCAACTCCTT TGCAAAACTT	42
a ia	AAGATAATTA AAGGAGATAT TGAGGATGCC GACTGCTTTA GGTTATTTGC ATTANACAAT	48
-26	AAACGCCCGT GAAATGGAAA TCATGCAAAG CTTTGCATGG AGAATATGTT NATAGAGATA	540
(ps	GACATGAAGA CATGAATATG CTTTCTTGAT GAACAACGAT GTTCACNTGT TTACTGCATG	600
35 U	CATGATACAT CCAATGTTCT AGGCTTGTTG GCAATCATTT TATTCNAAAA ATTGTCTGTT	660
40	TCTCTNCCNC CATAAGGTTA GCTTGTGGAA AATGTTCAAC TTTGGGCNCA NATGATCCGT	720
•	TTTAGCAAAA TCCCNCCATT CCTATTTTTT TCCGGAATCC NNTTGGNAAA ANATCCTNAC	780
	ATACTATTTC CACA	794
45	(2) INFORMATION FOR SEO ID NO: 53:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 798 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
55	(ii) MOLECULE TYPE: cDNA	
	(vii) IMMEDIATE SOURCE: (B) CLONE: U-D65	
60		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:	
.0	GGCACGAGGC CCGTAGAGCG AGTGCTGAGA TGGCTTTGAG GGCCTTCTTC CCCCTCTGCA	60
65	TCGCTCTCGT GGTGACGCTC TCACCTCTGT GTGATGCCAC TTCGCCTTAC TACACCATCA	120
	CACCGCCCAC CCCCGTGGCC AAGCCGCCTT CAGTTGAACC ACCACCCTAC CACGGCCCTC	180
70	CGACGACCCA CCCTAAGCCA CCGAGTCATG GTGGCCAACC TCCGTCCCAC CATCACCCAA	240

	CACCAATCTA CGGTGCACCC CCTCCGCAAC ACCACCACCA CCACCAACAC CACCACCAAC	300
	CTGCACCACC AACTCACGCA GAACACCCTC CGTACTACCA CATGCCTTCC CCGCCGCCGC	360
5	ATGGCCAGCA CCCGTCACCATG ATTATCCCGT ACCTCCTGCT CACAAGCCCC	420
	GAACTCCGCC GCCGGTTTAC AAGTCTCCAC CACCGACCCA CCGTCCTTAC CCTCCATCGA	480
10	CGCCACCCCA CCATCCGACG CACCCGCCTT CTCAGCCGAC GCCGTCATAC AAGGCCCCGC	540
10	CACCATACAA GAACATCCCT GANCATCTCC ACCGCCGCGT CACTATCATT CTCCGTCTTC	600
	ACCACCANCA CAACCACCAT NCAAATAGTC TCGTTTGCAT CTCTCCGTTG AANATGAACC	660
15	AATGTCNTTT AATAACGATC AGGGTTTCAA ATAAAAACNA ATTTCCGCCA TTGTAATGCT	720
	ATGGTTGTTC TCTCTGCTTC CCGGGGAAAG TTTCTTGGGT CATNTTAACC NCCTCCTAAT	780
20	GTTCNGCTCT TNNTANAA	798
20 f=1	(2) INFORMATION FOR SEQ ID NO: 54:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 824 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown 	
[() [() 30	(ii) MOLECULE TYPE: cDNA	
	(vii) IMMEDIATE SOURCE: (B) CLONE: U-D84	
() 35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:	
	GGCACGAGCG CCCACCCCG TGGCCAAGCC GCCTTCAGTT GAACCACCAC CCTACCACGG	60
40	CCCTCCGACG ACCCACCCTA AGCCACCGAG TCATGGTGGC CAACCTCCGT CCCACCATCA	120
	CCCAACACCA ATCTACGGTG CACCCCCTCC GCAACACCAC CACCACCACC AACACCACCA	180
45	CCAACCTGCA CCACCAACTC ACGCAGAACA CCCTCCGTAC TACCACATGC CTTCCCCGCC	240
	GCCGCATGGC CAGCACCGTC ACATGATTAT CCCGTACCTC CTGCTCACAA	300
60	GCCCCGAACT CCGCCGCGG TTTACAAGTC TCCACCACCG ACCCACCGTC CTTACCCTCC	360
50	ATCGACGCCA CCCCACCATC CGACGCACCC GCCTTCTCAG CCGACGCCGT CATACAAGGC	420
	CCCGCCANCA TNCNAGACCA TCCCTTGAGC ACTTCTCCAN CGNTTGCGTT TATTATCATT	480
55	CTCCGTCTTC ACCACCACCA CCACCACCAT ACAAATAGTC TCGTTTGCCA TCTCTCCGTT	540
	GAAGATGACG CAGTGTCGTT TTAGTAGCGA TCAGGGTTAC CAATAAGAAC GATGTTGCCG	600
60	CCATTGTAAT GGCTATGGTT GTTCTCTCTG CTTTTCCGGG GGAAGGTTCT TTGGGTTCAT	660
00	GTTAAACCTC TCTCTTAAAT GTTCATGCAT CTTATTATAA ACNAAAATTG GCCATTTNNN	720
	NNNTNTNNTN NNNNNTTNNN NNNNNAAAAC TCNAAAAATA TTTTTAAAAA CGGGCGGGGG	780
65	GCCCATCNAT TTTCCNNCCC GGGTNGGGGN TCCCAGNTTA TTNT	824
	(2) INFORMATION FOR SEQ ID NO: 55:	

⁽i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 797 base pairs
(B) TYPE: nucleic acid





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		(C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
	5	(ii) MOLECULE TYPE: cDNA	
		(vii) IMMEDIATE SOURCE: (B) CLONE: U-D75	
	10		
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:	
		GGCACGAGGG TTACGATCGT CATGTTGGGG GTGTTCAGCG GGGNAGGTGG TGGAGGTGCC	6
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	15	GGCGGAGCTG GTGGCCGCCG GCAGCAGGAC GCCGTCCCCT AAGACACGAG CGTCGGAGCT	12
		GATCAACCGA TTCCTCGGGA GCTTCGCTCC CGCGGTGTCG ATCCAGATCG GGGACTTGGG	18
	20	ACACCTCGCC TACTCCCACG CCAACCAGTC CCCCTTCGCT CCCAGGTTGT TTGCAGCGAA	240
		GGACGANATT TACTGCCTCT TCAAGGGAGT GCTGACCAAC CTGGGCAGCT TGAGGCAGCA	300
4mh 4mh 4mh	26	GTATGGGCTT TCCAAGAGTG CCGACNAGGT GGTGCTGGTC ATCGAAGCCT ACAAGGCCCT	360
Han gan	25	CCGTGACCGA GCTCCCTATC CTCCCAGCTT CATGCTCGCA CACCTTACTG GCAACTTCGC	420
ij		CTTCGTGCTC TTCGACAAGT CCACATCATC CATCCTTGTT GCATCTGACC CANATGGAAN	480
(1) ===	30	ANTACCCTTG TTCTGGGGGA TCACTGCANA TGGATGCCTT GCCTTTGCTG ACNATCTANA	540
į		CTTGCTGAAG GGATCGTGCG GGAAGTCACT TGCACCATTC CCTGAAGGAT GTTACTATTC	600
	25	CAATGCCTTG GGGGGCCTGA AAANCTATGA AAACCCCAAC ACAAGGTGAA CTGCTGTTTC	660
Hart Hart	35	TTGAANATGA AGAANAATTN TTTGTGCCNC TTTCAAGGTG GAANGATCTG CCNTTCTTGC	720
10 21 21		GGNAACCCCC TAATCAAGGA ACATCTTCCA ATGTTTGGGG CNAATGATCC TCTTAAAATC	780
	40	CTAAAATTCT TGGAATT	797
		(2) INFORMATION FOR SEQ ID NO: 56:	
	4.0	(i) SEQUENCE CHARACTERISTICS:	
_	-43	(A)-LENGTH: 804 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
	50	(ii) MOLECULE TYPE: cDNA	
	55	(vii) IMMEDIATE SOURCE: (B) CLONE: U-D83	
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:	
	60	GGCACGAGCT TCCACACAGG TGAGGGTAAG TCGGTTACGA TCGTCATGTT GGGGGTGTTC	60
		AGCGGGGAGG TGGTGGAGGT GCCGGCGGAG CTGGTGGCCG CCGGCAGCAG GACGCCGTCC	120
f		CCTAAGACAC GGGCGTCGGA GCTGATCAAC CGATTCCTCG GGAGCTTCGC TCCCGCGGTG	180
	65	TCGATCCAGA TCGGGGACTT GGGACACCTC GCCTACTCCC ACGCCAACCA GTCCCCCTTC	240
		GCTCCCAGGT TGTTTGCAGC GAAGGACGAN ATTTACTGCC TCTTCAAGGG AGTGCTGACC	300

AACCTGGGCA GCTTGAGGCA GCAGTATGGG CTTTCCAAGA GTGCCGACNA GGTGGTGCTG

	GTCATCGAAG CCTACAAGGC CCTCCGTGAC CGANCTCCCT ATCCTCCCAG CTTCATGCTC	420
	GCACACCTTA TTGGCAACTT CGCCTTCGTG CTCTTCGACA AGTCCACATC ATCCATCCTT	480
5	GTTTGCATCT GACCCANATG GAAAAATGCC CTTGTTCTGG GGGATCACTG CANATGGATG	540
	CCTTGCCTTT GCTGACNATC TANACTTGCT GAAGGGATCG TGCGGGAANT CACTTGCACA	600
10	TTCCCTGAAN GATGTTACTA TTCCAATGCC TTGGGGGGGC TGAAAANCTA TGAAAACCCA	660
10	ANCACAAGGT GACTGCTGTC TTGAANATAA AGAAAAATTT TTTGTGCCCC TTTCAAGGTT	720
	GAANGATCTG CATTCTTGCG GCACCCCCTN ATCNAGGAAC NTCNTNCCAA TGTTGGGGCA	780
15	AATATCCTCT TTAAAANCAT AAAA	804
	(2) INFORMATION FOR SEQ ID NO: 57:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 803 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
25	(ii) MOLECULE TYPE: cDNA	
]] []]] 30	(vii) IMMEDIATE SOURCE: (B) CLONE: U-D64	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:	
<u>ij</u> 35	GGCACGAGGG ATTATAAAAA GAAACTCGCA CTCAGCCAGA TTGACTCAAG CATGAAGGTT	60
1) 1)	GCATCTTTCG AATGTTCCTT TTTTTTCCAA CATCTTTTGA ATGTTACATG ACAATCATGA	120
40	CGCCGTGCAT ACAATGATAC CTCTGATAGG GTTGAATGCA CAAACCACTC ATCGTGCTAT	180
	ATTGCAAGTG CTTATGTTTG TATTCATTTT CTTATAATTT CAATGTGAGA GTTACCTTAG	240
	GTTCATATTA GATTTATATA ATATTGGGCA TAGATTTTTT TGTCATTGTT TGTGATCTGC	300
45	AATTTCATTA GGTCATCGAC CATATTATGG TAAATTTAAT TTACTAAATT ATATCTTGAG	360
	TTTATTGCTT TGCATATTTT GTGCTGGAAA CCATGCCAAT CCAACTCCTT TGCAAAACTT	420
50	AAGATAATTA AAGGAGATAT TGAGGATGCC GACTGCTTTA GGTTATTTGC ATTANACAAT	480
	AAACGCCCGT GAAATGGAAA TCATGCNAAG CTTTGCATGG AGAATATGTT NATAGANATA	540
	GACATGAAGA CATGAATATG CTTTCTTGAT GAACAACGAA GTTCACNTGT TTACTGCATG	600
55	CATGATACAT CCAATGTTCT AGGCTTGTTA GGCAACCTTT ATCCAAAAAA TTGTCTGTAC	660
	TCTCCCCCAT AAGGTAAGCC TGTGGAAAAT GTTCACTTTG GGCCNNATGA TCAGTTTANC	720
60	CGAAAATCCC CCTTCNTTAT TTGTTTTCTG AAACNCNTTG GAAANANATT CCTTACATAC	780
-	CTTTTTCACN NANATNTTGA ACC	803